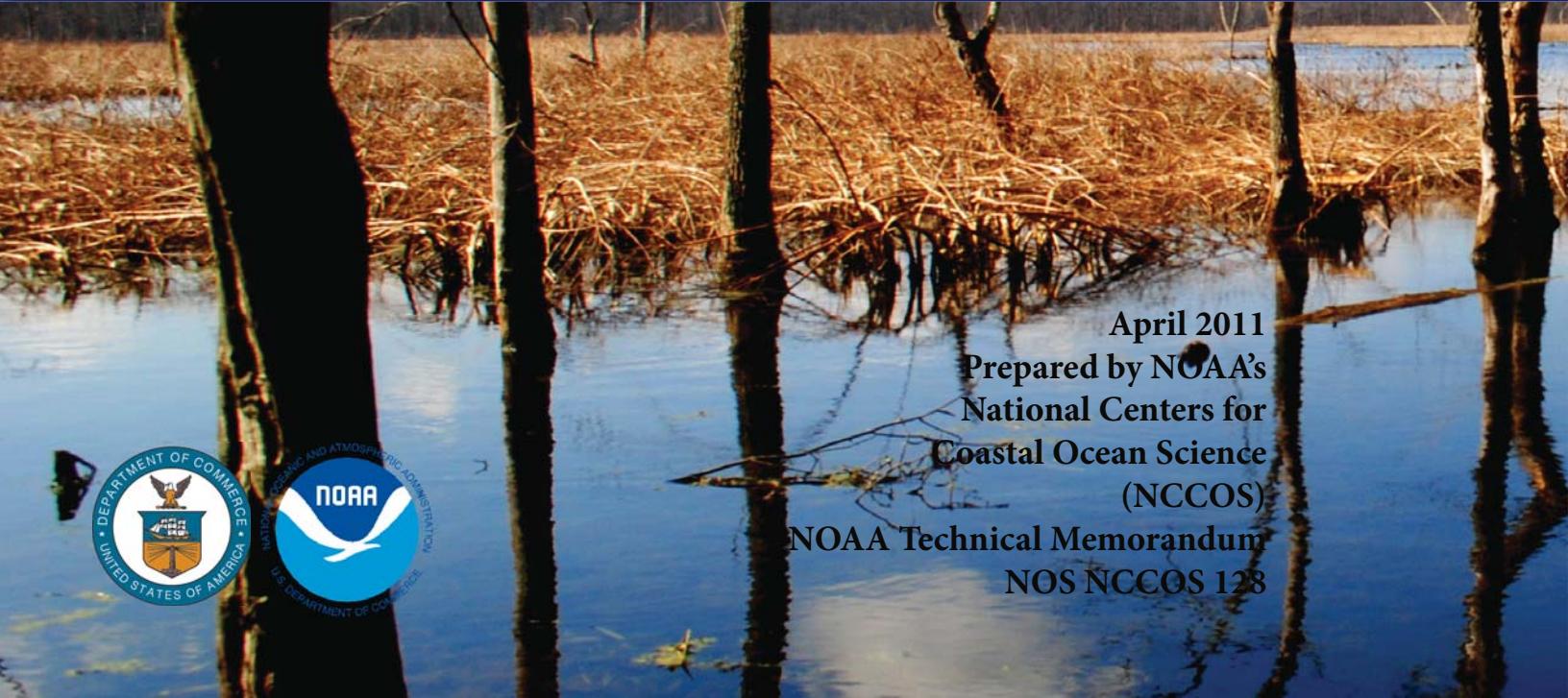




National Centers for Coastal Ocean Science (NCCOS) Research Highlights in the Chesapeake Bay

A.L. Mason, D. Apeti, and D. Whitall (eds.)





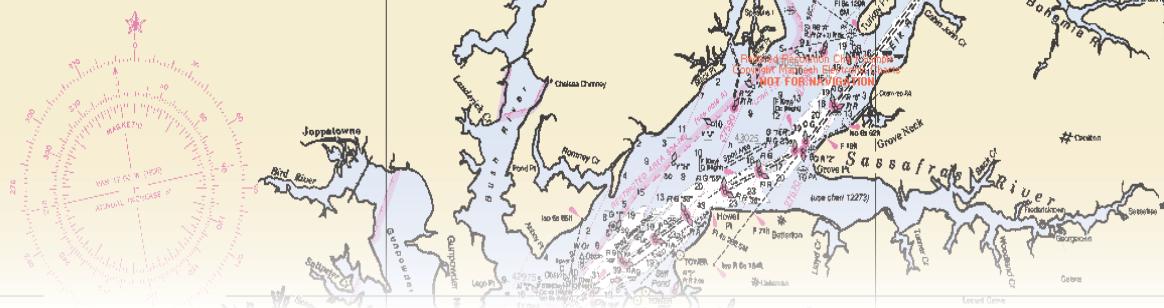
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UNITED STATES - EAST COAST
MARYLAND AND VIRGINIA

CHESAPEAKE BAY



National Centers for Coastal Ocean Science (NCCOS) Research Highlights in the Chesapeake Bay

A.L. Mason, D. Apeti, and D. Whitall (eds.)

Center for Coastal Environmental Health and Biomolecular Research (CCEHBR)
NOAA/NOS/National Centers for Coastal Ocean Science (NCCOS)
219 Fort Johnson Road
Charleston, SC 29412

Center for Coastal Environmental Health and Biomolecular Research (CCEHBR)
Cooperative Oxford Laboratory (COL)
NOAA/NOS/National Centers for Coastal Ocean Science (NCCOS)
904 South Morris Street
Oxford, MD 21654

Center for Coastal Fisheries and Habitat Research (CCFHR)
NOAA/NOS/National Centers for Coastal Ocean Science (NCCOS)
101 Pivers Island Road
Beaufort, NC 28516

Center for Coastal Monitoring and Assessment (CCMA)
NOAA/NOS/National Centers for Coastal Ocean Science (NCCOS)
1305 East-West Highway (SSMC-4, N/SCI 1)
Silver Spring, MD 20910

Center for Sponsored Coastal Ocean Science (CSCOR)
NOAA/NOS/National Centers for Coastal Ocean Science (NCCOS)
1305 East-West Highway (SSMC-4)
Silver Spring, MD 20910

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United States Department
of Commerce

Gary Locke
Secretary

National Oceanic and
Atmospheric Administration

Jane Lubchenco
Administrator

National Ocean Service

David Kennedy
Assistant Administrator

National Centers for
Coastal Ocean Science

Russell Callender
Acting Director





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Executive Summary



The Chesapeake Bay is the largest estuary in the United States. It is a unique and valuable national treasure because of its ecological, recreational, economic and cultural benefits. The problems facing the Bay are well known and extensively documented, and are largely related to human uses of the watershed and resources within the Bay. Over the past several decades as the origins of the Chesapeake's problems became clear, citizens groups and Federal, State, and local governments have entered into agreements and worked together to restore the Bay's productivity and ecological health. In May 2010, President Barack Obama signed Executive Order number 13508 that tasked a team of Federal agencies to develop a way forward in the protection and restoration of the Chesapeake watershed. Success of both State and Federal efforts will depend on having relevant, sound information regarding the ecology and function of the system as the basis of management and decision making. In response to the executive order, the National Oceanic and Atmospheric Administration's National Centers for Coastal Ocean Science (NCCOS) has compiled an overview of its research in Chesapeake Bay watershed.

NCCOS has a long history of Chesapeake Bay research, investigating the causes and consequences of changes throughout the watershed's ecosystems. This document presents a cross section of research results that have advanced the understanding of the structure and function of the Chesapeake and enabled the accurate and timely prediction of events with the potential to impact both human communities and ecosystems. There are three main focus areas: changes in land use patterns in the watershed and the related impacts on contaminant and pathogen distribution and concentrations; nutrient in-

puts and algal bloom events; and habitat use and life history patterns of species in the watershed.

Land use changes in the Chesapeake Bay watershed have dramatically changed how the system functions. A comparison of several subsystems within the Bay drainages has shown that water quality is directly related to land use and how the land use affects ecosystem health of the rivers and streams that enter the Chesapeake Bay. Across the Chesapeake as a whole, the rivers that drain developed areas, such as the Potomac and James rivers, tend to have much more highly contaminated sediments than does the mainstem of the Bay itself. In addition to what might be considered traditional contaminants, such as hydrocarbons, new contaminants are appearing in measurable amounts. At fourteen sites studied in the Bay, thirteen different pharmaceuticals were detected. The impact of pharmaceuticals on organisms and the people who eat them is still unknown. The effects of water borne infections on people and marine life are known, however, and the exposure to certain bacteria is a significant health risk. A model is now available that predicts the likelihood of occurrence of a strain of bacteria known as *Vibrio vulnifucus* throughout Bay waters.

Nutrients enter the Chesapeake through a variety of ways, including the outflows of wastewater treatment plants and in the runoff from agricultural fields, lawns, and road surfaces. The addition of excess nutrients causes algae, particularly phytoplankton, to bloom in much greater numbers than is normal. These bloom events can be merely a nuisance or they can cause significant problems in terms of both Bay and human health, depending on the scale of the event and the bloom spe-

cies involved. The Chesapeake is more heavily affected by eutrophication, an overabundance of nutrients, and increased algal growth, than are most American estuaries. As the blooms of algae die off, they decompose and create areas of low or no oxygen, usually in deeper Bay waters. These human induced events have become common and have played a major role in the decline of the Bay. The Chesapeake Bay Regional Ocean Modeling System (ChesROMS) indicates daily harmful algal bloom conditions for the Bay along with three-day forecasts of future conditions, allowing for a better understanding of where low oxygen areas may develop or where potential health risks related to algal bloom events may occur.

Changes in the Bay watershed have implications at all levels of the ecosystem. Fast swimming predators, such as striped bass (*Morone saxatilis*), need readily available oxygen to fuel their bursts of energy. The amount of available oxygen and temperature of the water are the primary factors in determining striped bass habitat. Low oxygen in bottom waters and high temperatures near the surface restrict striped bass to narrow bands of the water column in summer months. A model is now available that uses the amount and timing of freshwater flowing into the watershed to predict the range of striped bass in a given season. Oxygen isn't the only factor impacting fisheries populations. Menhaden (*Brevoortia tyrannus*) is important both as a food fish for predators such as the striped bass and as a commercial species, primarily used for fish meal and oil. Populations have steeply declined in recent years. The causes are linked to fishing, heavy predation by other fish, climate variability, and availability of their food. It is critical to understand organisms' patterns of movement and habitat use within the Chesapeake to be able to determine the causes of changes in their population levels. Annual patterns of habitat use are now available for 61 species of animals that inhabit the Chesapeake, all in one searchable location. This information has been useful in the designation of Essential Fish Habitat (EFH) and Environmental Sensitivity Index (ESI) mapping, tools used in the permitting process for development around the Bay and in the response to events, such as oil spills.

This document summarizes a sampling of research conducted by NCCOS scientists in the Chesapeake Bay watershed. For more information about NCCOS' contribution to Chesapeake Bay science please visit the NCCOS web site: <http://coastalscience.noaa.gov/>.

For more information about any of the projects listed here, please refer to the full publication cited in each chapter, or contact the lead scientist of a given project.

Introduction



Encompassing a 64,000 square mile watershed that extends from upstate New York to southern Virginia and from the West Virginia panhandle to the Delmarva Peninsula, Chesapeake Bay is the largest estuary in the continental United States. Historically, the Bay has been a very productive ecosystem that provides habitats for thousands of species and supports diverse human activities and economies. In the centuries since European settlement, population growth, development, and changes in land and water use within the Bay's watershed have caused pollution, changes in sedimentation patterns, and habitat degradation that have reduced the system's productivity. Oysters have been reduced to about 1% of their historic populations and fish kills, harmful algal bloom events, and hypoxic water conditions are now regular occurrences. Despite considerable efforts by Federal, State, and local agencies, Chesapeake Bay water quality has not substantially improved system-wide and the "fishable and swimmable" goals of the Clean Water Act (section 101(a)(1)) are yet to be attained. Based on current conditions and levels of effort, the restoration of the Chesapeake Bay and its watershed is not expected for many years.

Recognizing the ecological, economic and societal importance of Chesapeake Bay and acknowledging the need of an increased effort to save this vital ecosystem, the White House issued Executive Order (EO) 13508 in 2009. The EO describes Chesapeake Bay as a national treasure and ushers in a new era of Federal leadership, action, and accountability in the sustainable restoration of function and habitat to Chesapeake Bay. The National Oceanic and Atmospheric Administration (NOAA) is taking a lead role in the implementation of the EO, particularly in the areas of coastal spatial planning, climate research, and the restoration and

monitoring of habitats and living resources.

NOAA's National Centers for Coastal and Ocean Science (NCCOS) monitors and conducts research into the health and function of our nation's coastal and marine waters, including Chesapeake Bay. For more than two decades NCCOS has gathered unique sets of Chesapeake Bay data and conducted research on a diverse array of topics including pollution, eutrophication, occurrence of disease in estuarine organisms, climate and anthropogenic effects on living resources and their habitat, harmful algal blooms (HAB), and human dimensions. This research provides highly valuable baseline information that can be used in the attainment of the goals laid out in the 2009 EO through the direct support of ecosystem based management and serve as the basis for future research to address environmental concerns in Chesapeake Bay.

This report is a compilation of work conducted by NCCOS scientists on Chesapeake Bay and presents studies on habitat assessment, environmental monitoring, human dimensions, and water quality modeling.

INTRODUCTION



ECOSYSTEM



CHAPTER 1:

Chesapeake Bay Ecosystem

Assessment Program



Cooperative Oxford Laboratory
National Centers for Coastal Ocean Science,
Center for Coastal Environmental Health and Biomolecular Research

*Corresponding author, john.jacobs@noaa.gov, 410-226-5193 (phone), 410-226-5925 (fax)

BACKGROUND

There is universal recognition that land use affects many characteristics of receiving waters. For example, the practice of irrigation for agriculture or municipal water withdrawals influences hydrology and in-stream flow, and thus alters habitat availability (Van Sickle *et al.* 2004). Urbanization generally leads to increased concentrations of chemical contaminants (Comeleo *et al.* 1996), alterations in the direction and magnitude of stormwater flow (Klein 1979), and subsequent impairment of water quality (USEPA 1995). The effects of these land use choices on the ecology of the adjacent ecosystem is complicated, due in large part to the diffuse nature of non-point sources, buffering capacity of the land, and the natural variability of ecosystems in general (Paul *et al.* 2002). However, understanding these impacts is central to effective ecosystem management.

The concept of ecosystem indicators has received considerable attention in recent years as a means of describing ecosystem health or change by assessing biotic and abiotic factors. Several programs have been developed to provide these descriptions at regional or national scales. The U.S. Environmental Protection Agency's Environmental Monitoring and Assessment Program (EMAP) was initiated in the 1980s to develop the science needed to conduct regional and national level assessments (USEPA 2002). The National Oceanic and Atmospheric Administration's (NOAA) National

Status and Trends Program has similarly monitored the health of our nations resources since 1984. This program employs both ecological indicators (relevance at the population, community, or ecosystem level) and biomarkers (individual, cellular, or sub-cellular level of change). In Chesapeake Bay, the Atlantic Slope Consortium recently completed an ecosystem assessment relying principally on ecological indicators with application on small sub watersheds (Brooks *et al.* 2006). By reducing the scale of assessment to the sub-watershed level, both local and regional impacts were examined.

These programs have served to define a suite of indicators appropriate for examining ecosystem level change over various scales that are useful to regional managers in describing the ecological health of the system. However, these programs are generally not designed to provide detailed information at the local, land use decision making scale. In addition, ecosystem indicators provide evidence of holistic change (i.e., fish community structure), but are less robust in their ability to associate change with specific causes, or predict the biotic impact of local scale land use change.

Adams *et al.* (2000) and Adams (2005) provide a conceptual framework for addressing these shortcomings through the use of biotic indicators. The underlying concept is that the variability in estuarine/coastal systems requires the use of multiple indicators at varying levels of organization and comparison to reference sites. These reference sites offers a baseline of current

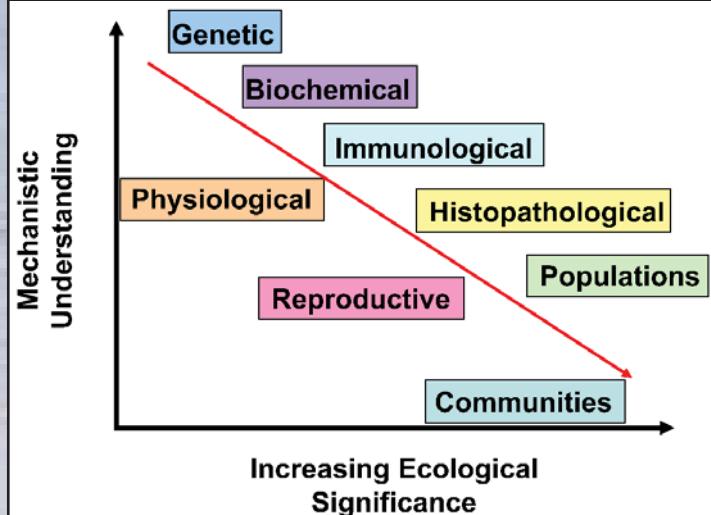
climatic and social conditions and obtainable goals for restoration in contrast to reliance on historical conditions. The hierarchical approach to sampling organisms from the sub-cellular level to populations provides resolution not possible with more typical community based approaches or those relying principally on abiotic factors. Stress is a departure from homeostasis in an organism and is the first stage of impairment. Identification of physiological stress may provide an early warning, and indicators at this level can be fairly specific for individual stressors (ex. acetylcholinesterase inhibition and pesticides). However, the ecological relevance of stress in an organism cannot be determined solely upon physiological change. Connecting changes at the sub-cellular level through pathological change in the organism to subsequent population level impacts allows for the realization of assessing the impact of specific anthropogenic influence on living resources, and subsequent ecosystem health (Figure 1).

Expanding on the conceptual framework of Adams *et al.* (2000) and Adams (2005), the choice of sentinel or indicator organisms is critical to the interpretation of results. Indicator organisms should possess the qualities of being ubiquitous in the systems of study and sensitive to the metrics examined. However, differing stressors impart differential response among species so that a single species model may not respond adequately to the signal presented. Thus, the use of multiple organisms occupying different ecological niches, and the application of hierarchical sampling to these species or groups could provide a broader picture while increasing the range of signal detection.

The National Oceanic and Atmospheric Administration states in its 2005-2010 strategic plan that a key objective is to “Protect, Restore, and Manage the use of Coastal and Ocean Resources through an Ecosystem Approach to Management (EAM).” This approach attempts to view an ecosystem in a holistic framework and incorporates all aspects of biological, climatological, and social data relevant to defining and quantifying ecosystem stressors and their impacts to allow for informed management decision making. In 2006, NOAA Cooperative Oxford Laboratory (COL) and federal, state, and academic partners initiated an ecosystem assessment with the intent of providing management relevant information on local scales by connecting the influence of land use sources to impacts on living resources. The specific objectives of the project are to:

- Evaluate linkages among land use, habitat qual-

Figure 1. Using multiple indicators over a range of biological levels of organization allows for inferences to be made from individual organisms to ecosystems (Adams 2005).



ity, and biotic health through the development and implementation of a multivariate ecosystem health indicator package;

- Demonstrate the utility of approach for ecosystem management through application to select Chesapeake Bay watersheds;
- Inform local decision making processes environmental impacts of changing land use patterns; and
- Transfer technology for application throughout Chesapeake Bay and other coastal systems.

APPROACH

Site Selection

For the initial development of the indicator package, site selection was based on the following criteria:

- Divergent land use characteristics and reference site;
- Small watersheds without extensive upstream hydrology (20-30,000 acres);
- Similar salinity range;
- Availability of historic and/or other monitoring data in system.

For site selection, sub-watershed boundaries (14 digit HOC) were overlaid on the National Land Cover Dataset (2001) to obtain comparative land use informa-

tion. Land use categories were combined into urban, forest, agricultural, wetlands, or barren for subsequent analysis. A total of 12 sub-watersheds in Maryland's Chesapeake Bay were included in the initial analysis, however 7 were subsequently excluded based on salinity range. Principal component analysis (S-Plus v. 8.0) was used to identify divergence in land use patterns. Three rivers were chosen from this process for an initial 3 year development program: the Magothy (38% urban), Corsica (70% agricultural), and Rhode (mixed use, 51% forested, 27% agricultural) rivers were selected.

Indicator Selection

Criteria for indicator application was based on the hierarchical approach of Adams *et al.* (2000) and Adams (2005) applied across multiple organisms (Figure 1). The principal organisms of interest include shellfish, fish, and bacteria. A generalized depiction of metrics measured in each organism or environment are provided as Figure 2. Detailed description of each bio-indicator and methods for determination are available in Messick *et al.* (*In Prep*).

Sampling Design

A random, stratified design was employed to fully characterize each sub-watershed. Stratification is accomplished by using the 6 foot contour to separate deep water from near-shore, shallow water habitats and river mile as a surrogate for salinity. Samples are also taken from upstream tributaries and the mouths of each system to provide source information and the influence of tidal flux. This approach allows for random characterization of the system as a whole, as well

as within system comparison. The stratification scheme divides each system into 9 blocks, and water quality and benthic characteristics for each block are represented by the sampling site. Organisms are collected within each river mile segment with appropriate block determined by the physiology or behavior of the organism (i.e., mummichogs tend to inhabit near-shore zones) for full analysis. All three systems are sampled during two week windows for direct comparison. Each location is sampled a minimum of three times per year, with community composition sampled every 3 weeks from June through October. The intensive sampling periods are based on mean water temperature to reflect spring conditions, maximum summer temperatures, and subsequent impacts in the fall.

KEY FINDINGS

(Demonstration Project) - While the intent of the three year demonstration project was to refine field and analytical approaches for the current effort, many interesting results emerged.

Water Quality

- The agricultural dominated Corsica River contained significantly higher nutrient concentrations (TN, TP) and turbidity ($p < 0.01$) than the other systems (Figure 3).
- Dissolved oxygen failed criteria for Chesapeake Bay (US EPA, 2003) 38% of the time in the Magothy River, 20% in the Corsica River, and 10% in the Rhode River.

Figure 2. Generalization of metrics chosen for application within each sub-watershed within the hierarchical sampling framework.

	Fish	Oysters	Clams	Crabs	Water	Sediment
Community Composition/IBI						
Habitat Quality						
Growth/Nutrition						
Disease Prevalence						
Contaminant Burden						
Parasite Burden						
Fertilizer/Pesticide Indicators						
Specific Pathogen Monitoring						
Immune Function Assays						
Endocrine Disruptors						
Stress Indicators						
Metallothionein Concentration						
Gene Expression						

Level of Organization



Benthic Condition

- Magothy River benthic habitats are in the poorest condition, particularly in tributaries and mid-channel stations (Figure 4).
- Metals and polycyclic aromatic hydrocarbons (PAHs) contributed the most of all measured compounds to the contaminant index, particularly zinc, mercury and arsenic (Leight *et al.* 2010).
- Toxicity from sediment exposure was greatest in the Magothy (43% of stations) and lowest in the Corsica (18% of stations).
- Benthic community condition (according to the Chesapeake Bay Benthic Index of Biotic Integrity) was poor at most stations, with 94% of stations in the Corsica possessing degraded benthos. Abundance, biomass, and species diversity were greatest in the Rhode River.

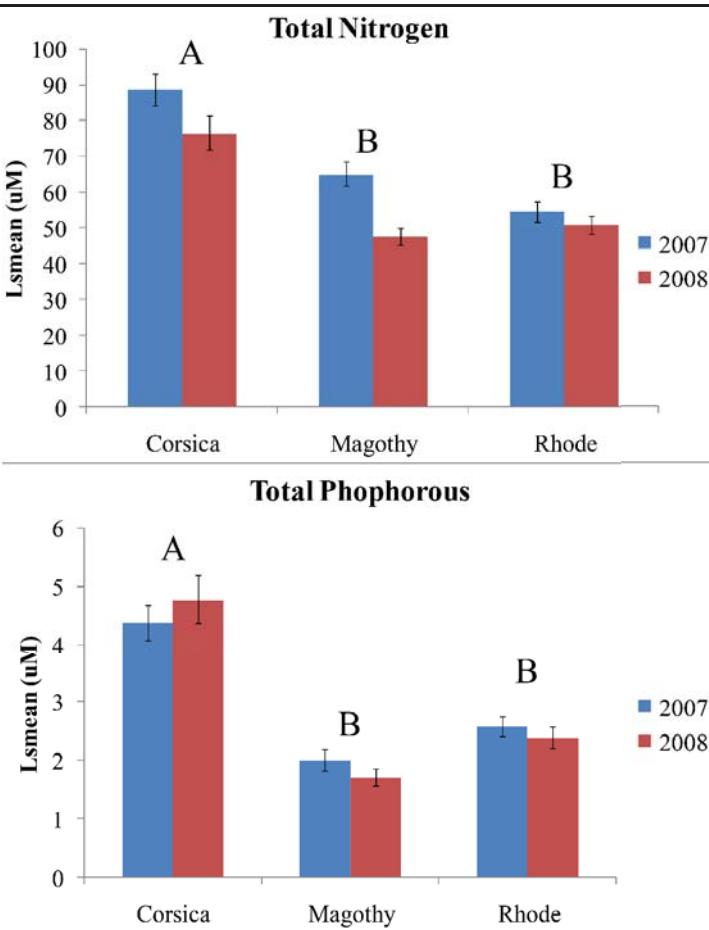
Bacteria

- The abundance of *Mycobacterium spp.* in the water was influenced by annual variability ($p = 0.01$) and river system with the agriculturally dominated Corsica River having significantly higher concentrations than the other systems ($p = 0.02$).
- Bacterial communities as measured by Automated Ribosomal Intergenic Spacer Analysis (16-23s) did not differ among river systems, but rather changed in response to season and salinity.
- Indicator bacteria densities exceeded state of Maryland bathing beach criteria 24% of the time in the Corsica River as compared to 14% and 2% in the Magothy and Rhode respectively.

Bioindicators

- The abundance and diversity of fish species was greater in the agriculturally dominated Corsica River than in the other systems ($p > 0.05$).
- The incidence of disease (Figure 5), density of macrophage aggregates and parasite burden in perch was also greater in the agriculturally dominated Corsica River ($p < 0.05$) while all measures of fitness

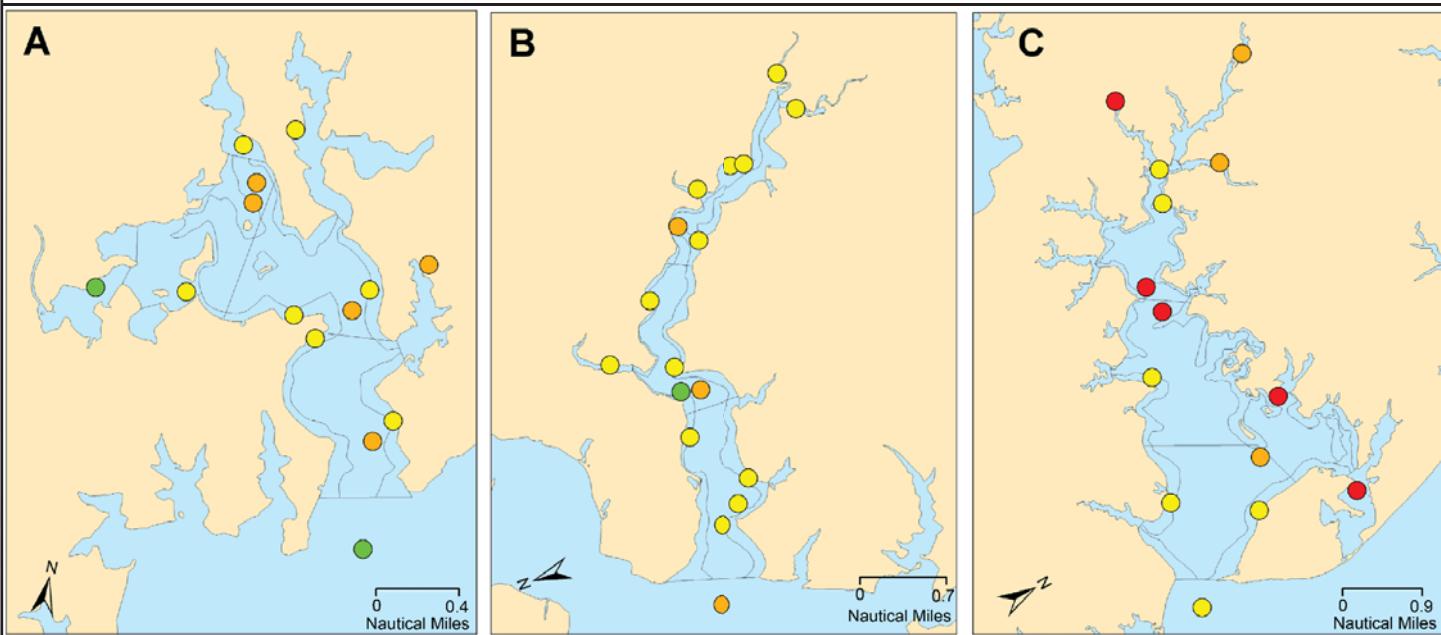
Figure 3. Total nitrogen and phosphorus concentrations by river and year. Same letter denotes lack of significance by river ($p < 0.01$).



or nutritional condition were reduced ($p < 0.05$).

- The incidence of inflammatory response in blue crab was also significantly greater in the Corsica River than the other systems ($p < 0.0001$). However, gill parasites were greatest in the mixed use system, the Rhode ($p < 0.0001$).
- Magothy River yielded the lowest catch per unit of effort (CPUE) for clams (*Macoma balthica*) and the highest Effects Range Median-Quotients (ERM-Q) for associated contaminants in benthic sediments ($p < 0.05$).
- All three systems contained little or no submerged aquatic vegetation, although the Magothy River contained the most with approximately 82 acres.
- Several indicators such as those targeting immune function, RNA:DNA ratios in white perch, and several histopathology indicators in blue crab were demonstrated to be redundant or to have little dis-

Figure 4. Benthic Condition Index results for sample stations in the Rhode (A), Corsica (B), and Magothy (C) Rivers. Results are based on a combination of B-IBI, chemical contaminant, and toxicity scores. Colors represent the number of degraded indices at each station (green = none, yellow = 1, orange = 3, and red = 3).



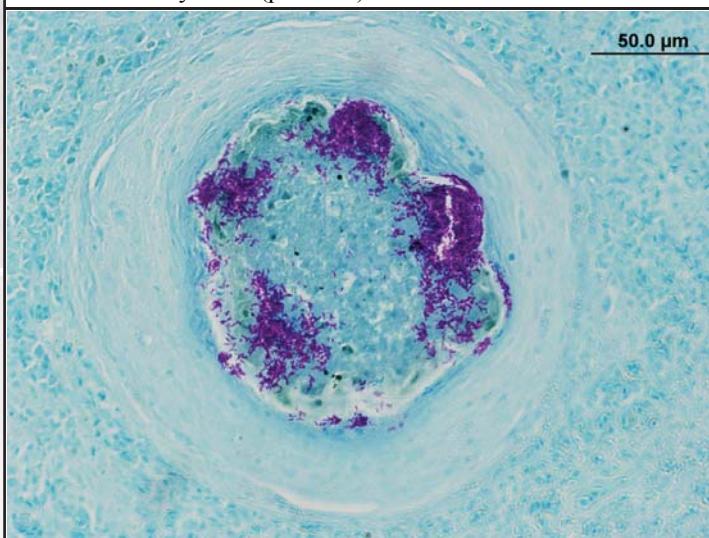
crimatory power.

- For most organismal metrics, the Fall season represented the most significant expression and allowed for the greatest discriminatory power among systems.

CONCLUSIONS

The findings of this initial effort are beginning to highlight the trade-offs that may exist in ecosystem approaches to management. For example, the agriculturally dominated Corsica River has characteristically

Figure 5. Granulomatous inflammation in a white perch spleen characteristic of mycobacteriosis. Over 45% of perch in the Corsica River tested positive for this disease, significantly greater than the other systems ($p < 0.01$).



elevated nutrient concentrations which may support a productive and diverse aquatic community. However, the health indicators of many of the species are generally poor in comparison to other systems. Conversely, the health of non-benthic organisms in the developed Magothy River is generally good, but benthic habitat is poor and higher in contaminants (Leight *et al.* 2010). This three year study demonstration served to help further refine the hypothesis and approach for this program and has provided valuable insight into the potential costs to ecosystem goods and services that land use decisions may incur. A refined approach is currently being applied to six systems within Chesapeake Bay (Figure 6) with future expansion planned to address larger scale land use and modeling needs.

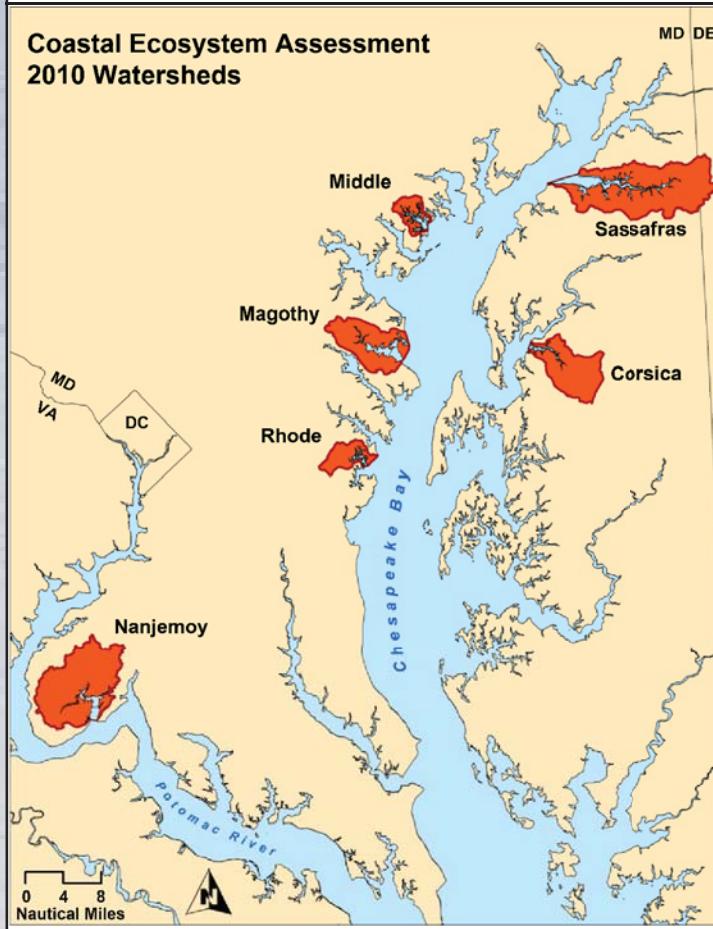
ACKNOWLEDGEMENTS

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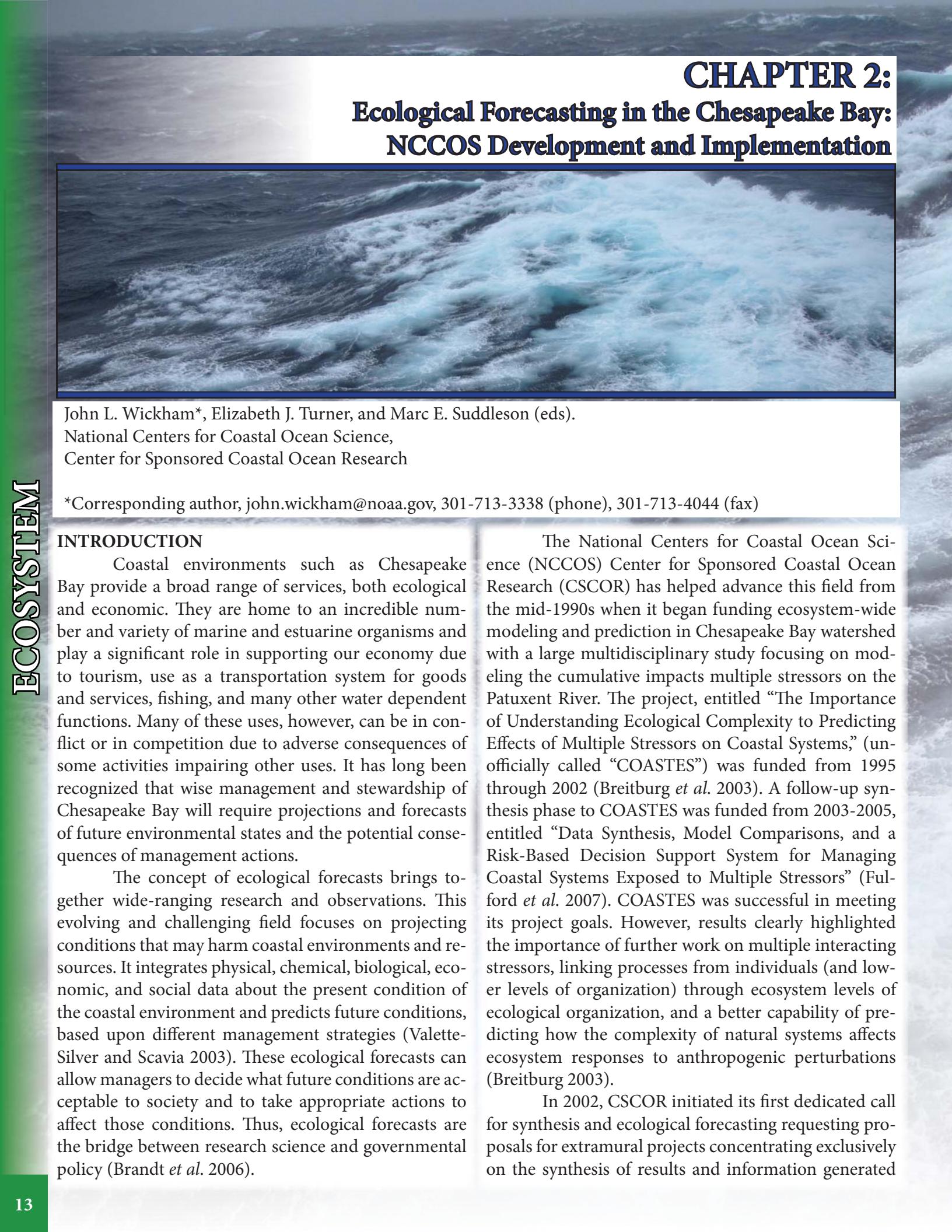
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CHAPTER 2: Ecological Forecasting in the Chesapeake Bay: NCCOS Development and Implementation

John L. Wickham*, Elizabeth J. Turner, and Marc E. Suddleson (eds).

National Centers for Coastal Ocean Science,
Center for Sponsored Coastal Ocean Research

*Corresponding author, john.wickham@noaa.gov, 301-713-3338 (phone), 301-713-4044 (fax)

INTRODUCTION

Coastal environments such as Chesapeake Bay provide a broad range of services, both ecological and economic. They are home to an incredible number and variety of marine and estuarine organisms and play a significant role in supporting our economy due to tourism, use as a transportation system for goods and services, fishing, and many other water dependent functions. Many of these uses, however, can be in conflict or in competition due to adverse consequences of some activities impairing other uses. It has long been recognized that wise management and stewardship of Chesapeake Bay will require projections and forecasts of future environmental states and the potential consequences of management actions.

The concept of ecological forecasts brings together wide-ranging research and observations. This evolving and challenging field focuses on projecting conditions that may harm coastal environments and resources. It integrates physical, chemical, biological, economic, and social data about the present condition of the coastal environment and predicts future conditions, based upon different management strategies (Valette-Silver and Scavia 2003). These ecological forecasts can allow managers to decide what future conditions are acceptable to society and to take appropriate actions to affect those conditions. Thus, ecological forecasts are the bridge between research science and governmental policy (Brandt *et al.* 2006).

The National Centers for Coastal Ocean Science (NCCOS) Center for Sponsored Coastal Ocean Research (CSCOR) has helped advance this field from the mid-1990s when it began funding ecosystem-wide modeling and prediction in Chesapeake Bay watershed with a large multidisciplinary study focusing on modeling the cumulative impacts multiple stressors on the Patuxent River. The project, entitled “The Importance of Understanding Ecological Complexity to Predicting Effects of Multiple Stressors on Coastal Systems,” (unofficially called “COASTES”) was funded from 1995 through 2002 (Breitburg *et al.* 2003). A follow-up synthesis phase to COASTES was funded from 2003-2005, entitled “Data Synthesis, Model Comparisons, and a Risk-Based Decision Support System for Managing Coastal Systems Exposed to Multiple Stressors” (Fulford *et al.* 2007). COASTES was successful in meeting its project goals. However, results clearly highlighted the importance of further work on multiple interacting stressors, linking processes from individuals (and lower levels of organization) through ecosystem levels of ecological organization, and a better capability of predicting how the complexity of natural systems affects ecosystem responses to anthropogenic perturbations (Breitburg 2003).

In 2002, CSCOR initiated its first dedicated call for synthesis and ecological forecasting requesting proposals for extramural projects concentrating exclusively on the synthesis of results and information generated

by coastal ecosystem studies that were concluded, or are near completion. The overall goal was to advance predictive capabilities, i.e., ecological forecasts. This was a key milestone in efforts to shape NOAA. A second ecological forecasting call followed in 2004 for the specific purpose of developing an ecological forecasting capability. In 2006, coordinating with NASA, CSCOR solicited a new call (“ECOFORE”) for forecasting capabilities to be developed, and for mature forecasts to be applied or transitioned to management uses.

In conjunction with the ECOFORE Program, several CSCOR Programs authorized by the Harmful Algal Bloom and Hypoxia Research Control Act (HAB-HRCA) of 2004 (Public Law 105-383) are charged with assisting coastal managers to mitigate the impacts of HAB events. The focus is on the development of predictive systems that are often based on ecological forecast models. In Chesapeake Bay, CSCOR has supported multi-year, interdisciplinary research studies to explore the factors that regulate the dynamics of HABs and how they cause harm, develop molecular methods for better identification and detection of harmful organisms, and advanced tools for continuous, real-time detection of HAB-related environmental parameters critical to HAB forecasting. In 2005, the CSCOR Monitoring and Event Response for Harmful Algal Bloom (MERHAB) research program initiated an effort to build and demonstrate a capability for operational HAB forecasts in Chesapeake Bay. This HAB forecasting program built on the existing sea nettle modeling advances and approach supported via ECOFORE (described herein) and involved CSCOR partners in Maryland to ground truth predictions.

CSCOR's history of efforts in building awareness of the need for ecological forecasting in the science and management community, raising the level of NOAA capabilities, and investing in the science to develop and demonstrate forecasts valued by end users have resulted in at least three “product lines,” in the Chesapeake Bay region alone. These prime examples are being used in discussions within NOAA Line Offices centered on the development of operational ecological forecasting products. For example, the NOAA National Weather Service, National Satellite and Information Service, and Office of Oceanic and Atmospheric Research began and continue to contribute to research and operational implementation of ecological forecasting projects within NOAA. See Cloyd *et al.* (2007) for a description of NOAA National Ocean Service modeling priorities.

Three completed NCCOS CSCOR-sponsored ecological forecasting projects centered in Chesapeake Bay are described herein. Future sponsored extramural research plans regarding ecological forecasting are also briefly described. The research projects highlighted in this chapter are summaries; not detailed, data-rich descriptions of the research. The reader is encouraged to review the reference citations and contact program managers and principal investigators for details regarding project background, research approach, key findings and conclusions.

ESTUARINE VARIABILITY: PREDICTING ECO-SYSTEM RESPONSE

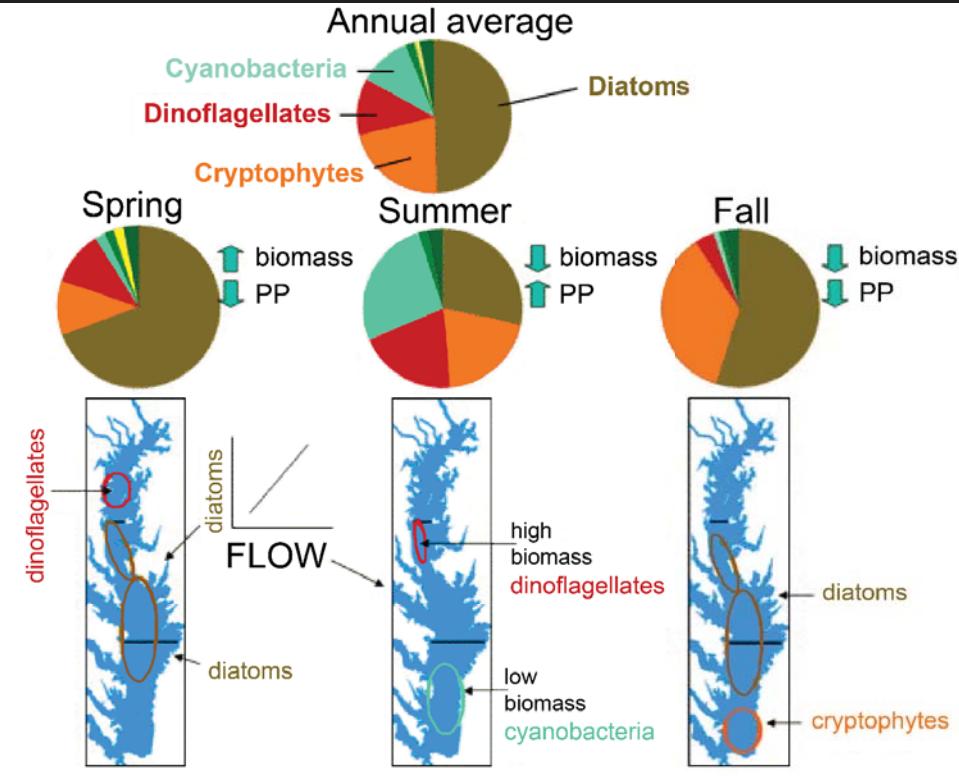
BACKGROUND

In 2002 CSCOR, under the initial ecological forecasting (ECOFORE) Federal Funding Opportunity, funded six, two-year proposals, one of which focused on the Chesapeake Bay region. The Chesapeake Bay proposal, entitled “Ecosystem Variability and Estuarine Fisheries: A Synthesis,” proposed to develop a series of forecasting tools to predict patterns and distribution of estuarine production, community composition and trophic structure at intra-annual, inter-annual and decadal time scales. These tools would provide a foundational platform to forecast the impact of both natural low-frequency climatic variability and anthropogenic changes on estuarine dynamics (Miller *et al.* 2006).

APPROACH

The foundation for the project's forecasts included a diverse range of historical information on water quality parameters from state and federal monitoring sources. The project made extensive use of the large U. S. EPA Chesapeake Bay Program Monitoring Database. At the core of the forecasting ability were two large, multidisciplinary research programs conducted by the principal investigators prior to the CSCOR award. The first being a NSF-funded project that sought to determine trophic interactions in ecosystem ecosystems sampling the variability and distribution of estuarine production at primary and secondary levels. The second being a fishery independent, multi species monitoring program funded by the NOAA Chesapeake Bay Office (Miller *et al.* 2006). The project imposed seven forecast modeling goals: 1) Patterns of timing and distribution of primary production, 2) regulation of zooplankton distribution, 3) distribution of fish and crabs, 4) variation in fish recruitment and production,

Figure 1. Conceptual summary of the spatial and temporal patterns of floral composition, Chl a, and PP. The top 'pie' is the annual long-term average floral composition (f_{chl-a}^{taxa}), with the seasonal long-term average combinations of floral composition, Chl a, and PP shown below. Areas of the Bay where recurrent blooms ($f_{chl-a} > 0.75$) were observed are shown with ovals, and regions where diatoms showed the greatest sensitivity to interannual variability of SRF, are shown on the maps for each season (from Adolf *et al.* 2006).



5) development of multispecies surplus production, 6) changes in fish community structure, and 7) forecasts of changes in ecosystem structure.

KEY FINDINGS

Patterns of Timing and Distribution of Primary Production

This task examined environmental forcing of floral composition, biomass as chlorophyll a (Chl a), and primary productivity (PP) of phytoplankton in Chesapeake Bay for six years (1995–2000). The goal was to describe regional, seasonal, and interannual variability in phytoplankton dynamics. Diatoms dominated the annual cycle, with seasonal contributions from cryptophytes, dinoflagellates, and cyanobacteria. Diatoms were positively influenced by Susquehanna River flow (SRF). The long-term average seasonal composition of Chesapeake Bay phytoplankton is disrupted by the influence of interannual variability of SRF, particularly in spring and summer. Phytoplankton community composition, Chl a, and PP respond predictably to environmental forcing associated with variability of SRF and attendant nutrient loading, affecting the function and fate of phytoplankton not conveyed by bulk measures

of biomass and productivity alone. (Adolf *et al.* 2006). Figure 1 shows a conceptual summary of this finding.

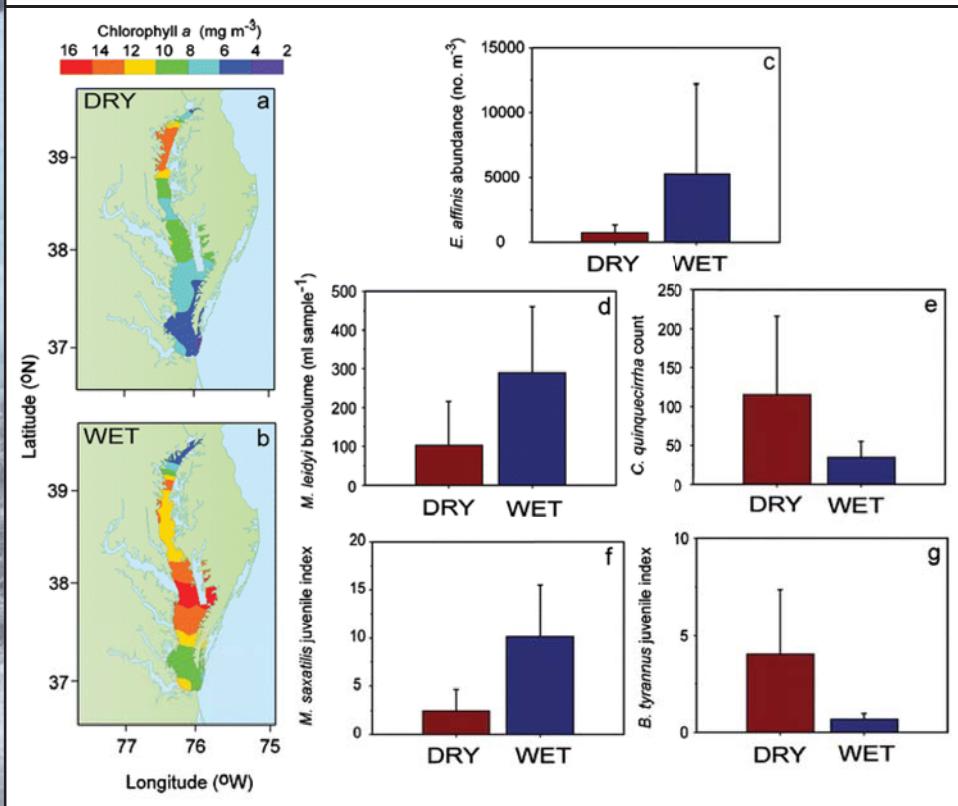
A synoptic climatology was developed for the eastern United States and used to quantify surface conditions affecting Chesapeake Bay during wet and dry years. This regional climatology was used to classify weather patterns that generate interannual variability in coastal and estuarine ecosystems. Wet and dry years were characterized by shifts in biogeography of Chesapeake Bay. The shifts resulted from habitat changes and trophic interactions and included the timing and magnitude of the spring phytoplankton bloom, the distribution/abundance of mesozooplankton and gelatinous zooplankton, and juvenile indices of fish. Synoptic climatology resolved regional weather variability at a spatial scale not strongly

controlled by larger-scale climate indices and explained ecosystem responses in Chesapeake Bay (Kimmel *et al.* 2009) (Figure 2).

Regulation of Zooplankton Distribution

Analyses of a 16 year time-series (1985–2000) of mesozooplankton abundance in Chesapeake Bay reveal the influence of freshwater flow on species composition and abundance. Trend analysis and linear mixed-effects regression models were used to assess long-term variation in, and influence of water-quality parameters (modulated by freshwater input) on the monthly mean abundance of the two dominant copepod species *Acartia tonsa* and *Eurytemora affinis*. There were no long-term trends in abundance of either copepod species, with the exception of a slight downward trend for *A. tonsa* in the mesohaline region of the northern Chesapeake Bay. Linear mixed-effects models showed a negative correlation between freshwater input and *A. tonsa* abundance in the oligohaline region, and no significant relationship between other water-quality parameters and *A. tonsa* abundance in the mesohaline region. *A. tonsa* abundance was positively correlated with temperature in the polyhaline region. *E. affinis* abundance

Figure 2. Biological response in dry and wet years. Spatial distribution of surface chlorophyll a (in milligrams per cubic meter) in Chesapeake Bay during dry years (a) and wet years (b) upper bay abundance of calanoid copepod *E. affinis* (number per cubic meter) (c), lobate ctenophore *M. leidyi* (milliliters of biovolume per sample) (d), scyphomedusan *C. quinquecirrha* (count) (e), striped bass *M. saxatilis* (juvenile index) (f), and Atlantic menhaden *B. tyrannus* (juvenile index) (g) during wet and dry years. Error bars represent the standard deviation (from Kimmel *et al.* 2009)



in the oligohaline region was negatively correlated with biovolume of the ctenophore *Mnemiopsis leidyi* and positively correlated with phytoplankton abundance. A negative correlation with salinity and a positive correlation with turbidity were found for *E. affinis* in the mesohaline region. Freshwater input appears to be mainly influencing habitat parameters specific to each copepod species and top-down control by predators (Kimmel and Roman 2004). Figure 3 presents a conceptual food web outlining these relationships.

Distribution of Fish

The project applied Generalized Additive Models (GAM) to develop forecasts of the distribution of all principal species in the National Science Foundation Trophic Interactions in Estuarine Ecosystems (TIES) database and the NOAA Chesapeake Bay Fishery-Independent Multispecies Survey (CHESFIMS) database and blue crab. Significant correlations were present among variables that affected blue crab distributions. Most notably, there was a strong and negative correlation ($r = -0.64$) between salinity and distance from the Bay mouth. Moderately strong correlations occurred

between salinity and temperature ($r = 0.34$), and between depth and bottom slope ($r = 0.28$) (Miller *et al.* 2006).

Variation in Fish Recruitments and Production

This task developed statistical models relating bay anchovy recruitments to dissolved oxygen, freshwater input from the Susquehanna River, spatial location of adult stock, and adult stock biomass. Recruitment levels from 1995-2004 survey data varied nine-fold; a peak recruitment of >250 billion anchovies was observed in 1998 (Figure 4). In the years of high freshwater flow in the months preceding the spawning season, adult anchovy stock remains primarily in the lower Bay region during summer and mostly spawns there. Under that condition, recruitments tend to be high, apparently a consequence of successful spawning and high larval

Figure 3. Conceptual model of a simple Chesapeake Bay food web. Arrows indicate flow of energy and numbers indicate mechanism levels (from Kimmel and Roman 2004).

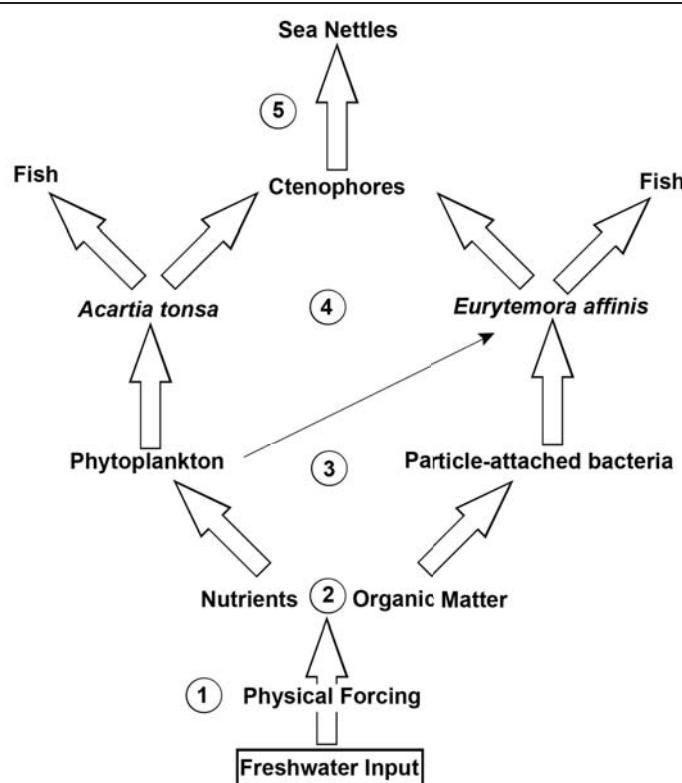
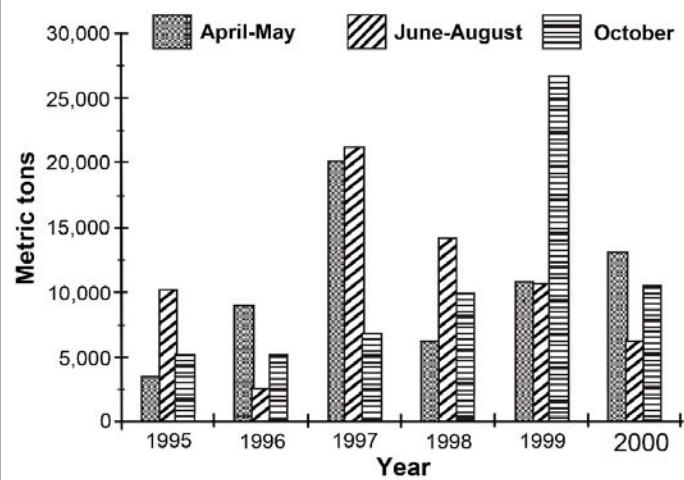


Figure 4. Baywide spawning stock biomass of bay anchovy in Chesapeake Bay from 1995 to 2000 (from Jung and Houde 2004)



production in the lower Bay region. Recruitment levels of bay anchovy from 1995 to 2000 were found to be inversely correlated with mean dissolved oxygen (DO) levels below surface layer during the summer months. This non-intuitive relationship is hypothesized to indicate a positive response to larval anchovy production during low DO years that is related to high plankton productivity, i.e., low mean DO is associated with high plankton production (anchovy prey) (Jung and Houde 2004).

Analysis of environmental factors indicated that water temperature and dissolved oxygen were important controllers of growth rate of bay anchovy. Inter-annual variability in length-specific mortality was inversely related to mean salinity in the summer and fall, suggesting that salinity controls abundance and spatial distributions of predators on bay anchovy. Results imply that annually variable hydrological conditions and secondary productivity may drive observed variability in recruitment and production of young of the year bay anchovy by inducing small but decisive differences in growth and predation mortality on early-life stages (Jung and Houde 2004).

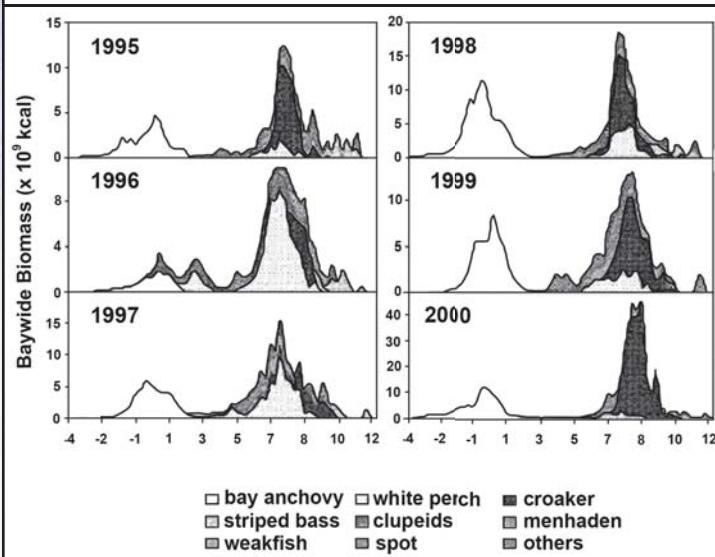
Biomass size spectra of pelagic fish were modeled to describe community structure, estimate potential fish production, and delineate trophic relationships in Chesapeake Bay. Spectra were constructed from midwater trawl collections each year in April, June-August, and October 1995-2000. The size spectra were bimodal: the first spectral dome corresponded to small zooplanktivorous fish, primarily bay anchovy *Anchoa mitchilli*; the second dome consisted of larger fish from several feeding guilds that are supported by multiple prey-predator linkages. Annual production estimates of

pelagic fish, derived from a mean production to biomass ratio, varied nearly three-fold, ranging from 162×10^9 kcal (125×10^3 tons) in 1996 to 457×10^9 kcal (352×10^3 tons) in 2000. Results suggest that fish size spectra can be developed as useful indicators of ecosystem state and response to perturbations, especially if prey-predator relationships are explicitly represented (Jung and Houde 2005) (Figure 5).

Development of Multispecies Surplus Production

The project analyzed catch per unit effort (CPUE) and overall catch data from 1982-2001. Benthivore (aggregate of Atlantic croaker, spot, summer flounder, channel catfish, and white catfish) and pelagic piscovore (aggregate of striped bass, white perch, bluefish, and weakfish) CPUE were similar with both guilds rising to a peak from 1981 to early 1990s and then stabilizing. Conversely, trends in catch diverged between the two guilds in the early 1990s, as benthivore yield nearly tripled between 1991 and 2001 whereas pelagic piscivore yield increased by only 70%. The dramatic increase in benthivore yield can be largely attributed to Atlantic croaker, whose catch increased from less than 1000 tons in 1991 to more than 10,000 tons in 2001. Production results revealed that the pelagic piscivore guild was near maximum sustainable yield in the late 1980s. When fishing mortality subsequently decreased in the early 1990s, piscivore biomass was 50% larger than maximum sustainable yield. Relative to the benthivore guild, however, the pelagic piscivore guild is currently much closer to its maximum sustainable yield

Figure 5. Annual spectra. Species composition of annual biomass size spectra of pelagic and benthopelagic fish in Chesapeake Bay (1995-2000). Clupeids includes *Alosa spp.* (shads and river herrings) and gizzard shad (*Dorosoma cepedianum*). Note the y-axis scales vary (from Jung and Houde 2005)



(Miller *et al.* 2006).

Changes in Fish Community Structure

The project assembled complete fisheries landings data by species and specific water body for the Potomac River and for the mainstem Bay (excluding tributaries) from 1981-2002. A considerable amount of interannual variability exists in total landings for both water bodies. For mainstem Chesapeake Bay, 89% of these landings were menhaden. The second and third ranked dominant species caught in the mainstem were blue crabs and Atlantic croaker, though both landings were together were ~ 10% of the total landings. From 1995-2001, total landings declined significantly for the mainstem Chesapeake Bay, while Potomac River land-

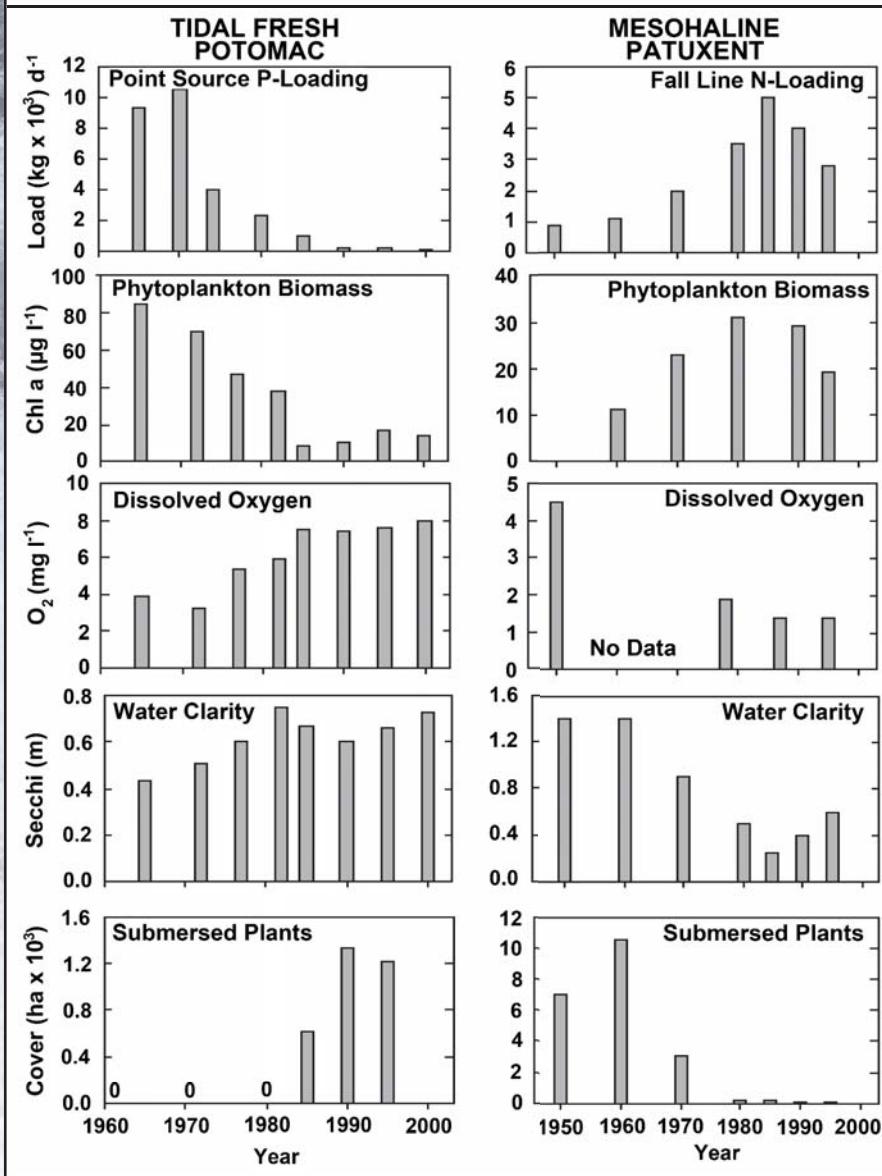
ings appeared to decline in the 1960s, and again after the mid-1980s. Dominant species caught in the Potomac River are striped bass, oysters and blue crabs. Though the dominance of each species has changed throughout the time period, blue crabs comprise the largest landings of any harvested species in the Potomac. Oysters and striped bass are also dominant species; though appear to be declining steadily throughout the landings record. The reduction in striped bass landings during the late 1980s was caused by a fishing moratorium on this species because of very depressed stocks.

Since the mid-1980s deep water dissolved oxygen levels have been depressed during warm months of all years and benthic habitat conditions have also been poor. These observations are consistent with de-

tailed studies indicating degraded benthic habitat under hypoxic conditions in this and other estuaries. However, the declining pelagic:demersal fish ratio (P:D ratio) (1995-2000) in the mainstem Bay is mainly the result of declining menhaden landings rather than further declines in demersal species. Using nutrient loading and fisheries landing data for the full Chesapeake Bay system Kemp *et al.* (2005) reported a distinct increase in the P:D ratio that was caused by both increases in pelagic catch and decreases in demersal catch. This pattern was accompanied by increasing nutrient loads, declining submerged aquatic vegetation communities, increasing algal stocks, intensification of hypoxic duration and extent and declines in the efficiency in the transfer of primary production to higher trophic levels. It is clear that both algal biomass and fisheries composition changed substantially during this 30 year period. It is observed that changes in fishery stocks and rates of harvest are tied to fishing preferences, fishing effort, market demands, fishing techniques and regulations as well as habitat, water quality and climate variability.

While signs of increased phytoplankton and decreased water clarity first appeared ~100 years ago, severe, recurring deep-water hypoxia and loss of diverse submerged vascular plants were first evident in the 1950s and 1960s, respectively. The degradation of these benthic habitats

Figure 6. Time-series plots of nutrient loads, phytoplankton biomass, dissolved oxygen, water clarity, submerged vascular plant biomass in tidal fresh portion of Potomac River estuary and mesohaline portion of Patuxent River estuary. Data are averaged for 5 or 10 year intervals (from Kemp *et al.* 2005)



has contributed to declines in benthic macrofauna in deep mesohaline regions of the Bay and blue crabs in shallow polyhaline areas. In contrast, copepods, which are heavily consumed in pelagic food chains, are relatively unaffected by nutrient-induced changes in phytoplankton. Although the Bay's overall fisheries production has probably not been affected by eutrophication, decreases in the relative contribution of demersal fish and in the efficiency with which primary production is transferred to harvest suggest fundamental shifts in trophic and habitat structures. Bay ecosystem responses to changes in nutrient loading are complicated by non-linear feedback mechanisms, including particle trapping and binding by benthic plants that increase water clarity, and by oxygen effects on benthic nutrient recycling efficiency (Kemp *et al.* 2005). Figure 6 shows a summary of changes in Chesapeake Bay community structure over a 40-50 year period to 2000.

Forecasts of Ecosystem-Level Changes

Although total fisheries harvest in the Bay has generally increased during the last fifty years, the mean trophic level of this harvest (as weighted mean trophic level of harvested animals calculated from a trophic network model on a scale from 2-3) has declined steadily from in the early 1950s to the late 1990s. Most of this changes occurred between 1950 and 1975. The pelagic fraction of fisheries production showed a radical shift in the 1950-1960 decade followed by a more gradual increase thereafter to 2000. Changes in menhaden harvest rates during this period have contributed substantially to these trends (Miller *et al.* 2006). During this same half century time-period, human populations and agricultural activities in the estuary's watershed have increased, resulting in generally increasing nutrient inputs to Chesapeake Bay. It appears that primary production has increased more rapidly than has fisheries harvest over this time period, such that the ratio of the fisheries to productivity has actually declined as nutrient enrichment increased in the estuary. This relationship suggests the possibility that trophic efficiency has declined with increased nutrient loading. To the extent that this is the case, the project results speculate that the increasing fraction of primary production is going to support activity of lower-level trophic level organisms (i.e., microbial decomposer communities).

Project model experiments revealed generally consistent patterns of responses to increased nutrient loading, where total phytoplankton and the ratio of large algal cells (e.g., diatoms) to small algal cells (e.g.,

phytoflagellates) tended to increase with nutrients, while consumer groups (e.g., oysters, crabs, fish, jellyfish) respond by initially increasing biomass with initial increases in nutrients but peak at modest nutrient loading rates. As a consequence, the trophic efficiency (defined as the ratio of consumer secondary production to producer primary production) tends to exhibit an initial increase at lower nutrient loading rates followed by a marked decline; consumer biomass does not respond to further nutrient-stimulated increases in phytoplankton. However, this relationship depends on the intensity of predation pressure from top consumer predators down to lower consumers and then producers. At low predation pressure, consumer biomass continues to increase with nutrients and there is little evidence of a leveling off of biomass, whereas consumer biomass peaks at intermediate nutrient levels when predation pressure is high. The overall pattern represents a "trophic cascade" of responses to nutrient loading as described by Carpenter and Kitchell (1993). Despite these trophic cascades, nutrient enrichment always produces consistent responses of trophic efficiency - first increasing, then peaking, and then decreasing - along an increasing nutrient enrichment gradient (Miller *et al.* 2006).

CONCLUSIONS

Overall, the relevance of the project model results for nutrient input reduction management strategies in coastal systems such as Chesapeake Bay will depend on the location of where these ecosystems are on their particular nutrient-fishing mortality response curve. If an ecosystem is saturated with regard to fish biomass then modest reductions in nutrient input will not affect potential fisheries stocks and production; if the system is near the peak or undersaturated on the nutrient-fishing mortality response curve, nutrient reduction could contribute to reduced fish production. There is potential for using biomass ratios (for example, large to small algal/phytoplankton to bacteria biomass) as indicators of the how close an ecosystem is to its peak fish biomass saturation point. It is hoped further analysis will bring more understanding of these relationships.

The project made substantial progress in developing predictive models of fish distributions and recruitment variability of fishes in Chesapeake Bay, especially bay anchovy and striped bass. The work validated the forecasting ability of the project models using testing and training datasets. The synoptic climatological approach employed has substantial potential for understanding physical controls on production and fore-

casting how climate change and other low frequency variation may impact levels of predation in the nation's estuaries (Miller *et al.* 2006).

PREDICTING NEAR REAL TIME DISTRIBUTION OF THE SCYPHOMEDUSA *CHRYSAORA QUINQUECIRRHA*

BACKGROUND

In 2004 CSCOR took another step in the development of ecological forecasting in soliciting proposals for the purpose of developing an ecological forecasting capability for selected issues. Under a 2004 Federal Funding Opportunity three proposals were selected, one of which focused on Chesapeake Bay. This proposal "Development of Operational Model for Predicting the Near Real Time Distribution and Abundance of the Scyphomedusa, *Chrysaora quinquecirrha*, in Chesapeake Bay" proposed to develop and implement an operational system to routinely generate daily nowcasts and 3-day forecasts of the probability of occurrence of the scyphomedusa *Chrysaora quinquecirrha*, commonly known as the sea nettle. Aspects of this project already existed in a research mode and were being developed for potential operations by NOAA National Satellite and Information Service Center for Satellite Applications and Research and National Ocean Service Office of Coast Survey and three academic partners (CSCOR 2011a). CSCOR's support has helped move the system towards operational status.

Sea nettles, *Chrysaora quinquecirrha*, seasonally infest Chesapeake Bay and affect many activities along its shores, including recreational activities. The effect of sea nettles is not limited to vacationers or weekenders who may shun Chesapeake Bay beaches to avoid painful allergic reactions from contact with their tentacles. Sea nettles are voracious predators, devouring copepods (minute crustaceans), fish eggs and larvae and comb jellies - thereby affecting the food web and possibly the abundance of fish in the Bay. The adverse effect of sea nettles may be mitigated if their presence can be monitored and predicted in near real time. Knowing where and when to expect this biotic nuisance may help people better plan their activities and eventually help to alleviate this problem (Trivedi 2002).

Chrysaora quinquecirrha medusae are important in the ecology of Chesapeake Bay. They can reach very high concentrations in the summer, particularly in the tributaries where concentrations of 16m^{-3} have been measured. This stinging jellyfish occurs in such great

abundance that methods were evaluated to control their population sizes 40 years ago. In particular, the medusae are extremely important to plankton dynamics due to their high trophic position in the Chesapeake Bay food web. The medusae consume significant amounts of copepods and bay anchovy eggs and larvae in Chesapeake Bay. As possible competitors for zooplankton prey with bay anchovy (*Anchoa mitchilli*) which is an important food for striped bass (*Morone saxatilis*), bluefish (*Pomatomus saltatrix*) and other species, medusae could have indirect impacts on commercially important fish populations. *C. quinquecirrha* also plays an important role as a control of the ctenophore *Mnemiopsis leidyi*, and can control ctenophore populations in part of Chesapeake Bay where the medusae reduced ctenophore abundance and copepod numbers increased. Thus, predation by *C. quinquecirrha* medusae has important and complex effects on the food web of Chesapeake Bay (Decker *et al.* 2007).

Over 700 *in situ* observations collected from Chesapeake Bay and its tributaries during 1987–2000 were used to develop habitat models that predict the probability of occurrence and the likely concentration of medusae as a function of sea-surface temperature and salinity. Medusae were found within a relatively narrow range of temperature (26 to 30°C) and salinity (10 to 16 ppt.). Regression analyses reveal that a combination of temperature and salinity is a significant predictor of medusa occurrence. Assessments of the predictive performance of these models using medusae and environmental data collected at independent survey sites ($n = 354$) indicated that model-predicted medusa occurrence and concentration correspond well with observations. The r models can be forced with near-real time



and retrospective estimates of temperature and salinity to generate probability of occurrence maps of *C. quinquecirrha* medusa presence and abundance in order to better understand how this top predator varies in space and time, and how this species could potentially affect energy flow through the Chesapeake Bay system (Decker *et al.* 2007).

APPROACH

The project used *C. quinquecirrha* as a model to examine physical factors that control jellyfish populations and to develop an ecological forecasting system. The project goals were to: (1) develop and refine habitat models to estimate the likelihood of occurrence and density of *C. quinquecirrha* medusa in Chesapeake Bay, (2) determine additional variables that define the “preferred” habitat of *C. quinquecirrha*, (3) validate habitat models derived for *C. quinquecirrha* in Chesapeake Bay, (4) conduct retrospective examinations of *C. quinquecirrha* distributions in Chesapeake Bay, (5) determine how climate changes may affect future *C. quinquecirrha* populations, (6) provide predictions of *C. quinquecirrha* for input into Chesapeake Bay ecosystem management models (Ecopath/Ecosim), (7) transition the hydrodynamic model from the CH3D system to a more adaptable community supported model, and (8) operationalize the *Chrysaora* prediction system.

KEY FINDINGS

The project developed and implemented a system and web site that routinely generates and stages nowcasts and 3-day forecasts of the likelihood of encountering *Chrysaora quinquecirrha* in Chesapeake Bay at the NOAA Chesapeake Bay Office. The nettle web

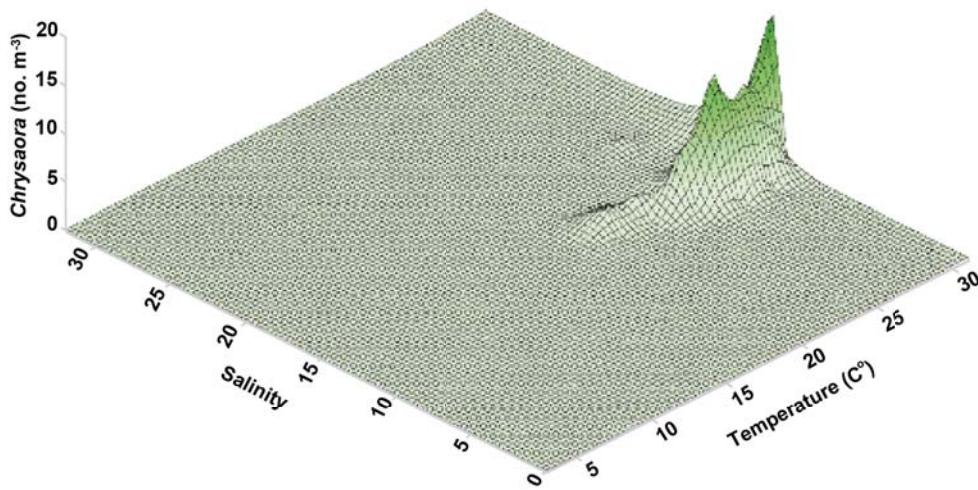
site graphically displays the sea nettle predictions. Nowcasts and 3-day forecasts of *C. quinquecirrha* probability of occurrence in the Bay are displayed, as well as the associated temperature and salinity fields in several commonly used formats, e.g., PNG, and Arc Info shapefiles, which can be easily imported into geographic information systems. (<http://chesapeakebay.noaa.gov/forecasting-sea-nettles>).

The project analyzed relationships between observed and predicted medusa presence in order to assess the reliability of predictions. Model-predicted probability of medusa occurrence corresponded well with observed medusa occurrence in the test dataset. Overall, 86.7% of the estimates were correctly predicted by the model. The proportions of observations misclassified by the model, specifically, the false positive and false negative rates, were 32.5 and 7.7%, respectively. Nowcasts of *C. quinquecirrha* probability, sea-surface temperature and salinity were compared against weekly in situ observations collected at two locations on Chesapeake Bay - the piers at Horn Point Laboratory and Chesapeake Bay Laboratory - over a six month period. When the likelihood model was forced with weekly observed sea-surface temperature and salinity occurrence likelihoods were similar to those predicted from modeled temperature and salinity.

Medusae were found within a relatively narrow range of temperature (26 to 30°C) and salinity (10 to 16 ppt.) (Figure 7). Regression analyses reveal that a combination of temperature and salinity is a significant predictor of medusa occurrence. Retrospective analysis suggests the timing of the appearance and disappearance of *C. quinquecirrha* in the Bay is dependent on temperature, while its distribution within the bay is

dependent on salinity (Decker *et al.* 2007). Maps generated by applying the habitat model to hindcast temperature and salinity fields predicted the distribution and likelihood of *C. quinquecirrha* medusa occurrence in Chesapeake Bay. Maps of the likelihood of medusa occurrence illustrate the evolution of the bloom through space and time and the patterns of *C. quinquecirrha* distributions can be examined with respect to environmental factors in order to examine the timing of appear-

Figure 7. Plot illustrating the salinity and sea-surface temperatures encompassing 95% of the sea nettle densities in surface waters of the Chesapeake Bay (from Decker *et al.* 2007)



ance and disappearance of medusae. Results also indicate that temperature and salinity have varying effects on the spatial distribution of medusae. In mid-season, salinity, which has a strong north-south gradient in summer is important in predicting where medusae are found in the Bay. By contrast, mid-summer surface temperature is uniform within Chesapeake Bay and has little apparent effect on the spatial distribution of *C. quinquecirrha* medusa.

Analysis of observations collected in the York River suggests that highest abundance of medusae in that river estuary occurs during June to August. Individual medusae are distributed primarily at the upriver stations, with small juvenile medusae present during early summer (approx. 10-30 mm bell diameter) and larger, mature medusae present during late summer (approx. 120-150 mm bell diameter). These stations are characterized by relatively low salinities (10-15 ppt.), and are located in areas where small creeks (Sarah and Aberdeen Creeks) feed into the York River. During 2006 sampling medusae were first observed in the tributaries and York River in mid-May and several medusae were collected at the upriver locations throughout June (Decker 2008).

CONCLUSIONS

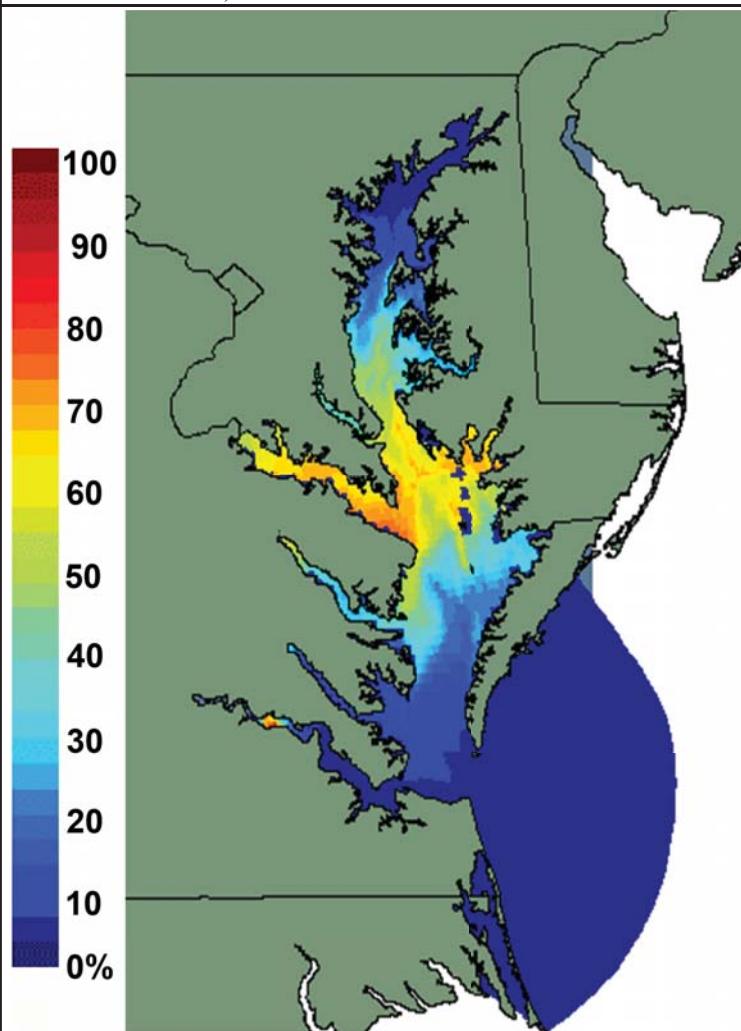
The project models and associated now-casting/hindcasting system provide insight into the factors that control temporal and spatial variability of *C. quinquecirrha* medusa in Chesapeake Bay because it allows for the examination of inter-annual and seasonal variability in medusa distribution and abundance. Maps of the likelihood of medusae occurrence routinely generated by the system illustrate the evolution of the bloom through space and time; the patterns of medusa distributions can also be examined with respect to environmental factors in order to examine the timing of appearance of medusa. The models, which employ temperature and salinity, predict the presence/absence and potential concentration of *C. quinquecirrha* medusa with reasonable accuracy, however comparison of weekly hindcasts and observations indicates that the likelihood of occurrence model predicts the peak of the medusa bloom well, but the model is less accurate in predicting the presence of medusa at the beginning and end of the bloom (Decker *et al.* 2007).

Daily nowcasts and 3-day forecasts of surface salinity, temperature and likelihood of encountering *C. quinquecirrha* in Chesapeake Bay are gen-

erated and staged daily for dissemination on the sea nettle website for interested agencies and the public to view. The most current nowcast, as well as information describing sea nettle life history, is staged on the operational website <http://chesapeakebay.noaa.gov/forecasting-sea-nettles> for dissemination. Users can view these data at various magnifications and in relation to local landmarks (Figure 8).

This NOAA effort is a major scientific achievement in ecological nowcasting and presenting environmental information and a useful tool in an area of ongoing research of broad economic and ecological importance. The project also represents a novel and exciting approach that combines real-time data derived from disparate sources, such as numerical circulation models, operational satellites, and moored sensor systems, to generate nowcasts and forecasts of the distribution pattern of noxious marine biota. Further efforts are ongoing to transition the sea nettle forecast to true operational status within NOAA.

Figure 8. Example prediction of the percent likelihood of encountering sea nettles, on 17 August 2007 in the Chesapeake Bay (from Aikman *et al.* 2010).



DEVELOPMENT OF AN OPERATIONAL HARMFUL ALGAL BLOOM PREDICTION SYSTEM

BACKGROUND

In 2005, CSCOR's Monitoring and Event Response for Harmful Algal Blooms Program (MERHAB) initiated a project centered in Chesapeake Bay. This 5-year effort, entitled "Development and Implementation of an Operational Harmful Algal Bloom Prediction System for Chesapeake Bay," had a primary goal to develop and implement an operational harmful algal bloom prediction system for Chesapeake Bay and its major tributaries. Co-investigators at the Maryland Department of Natural Resources are building these products into their plans to improve their HAB response and monitoring capabilities (CSCOR 2011c). This project built on the previously described sea nettle forecast system and has been expanded to include prototype models for biogeochemicals, hydrodynamics, habitats, HABs and pathogens under development for Chesapeake Bay. Coupling and integration of these models into a unified ecological prediction system is a long-term goal (Brown 2011, personal communication).

APPROACH

The variety of harmful algal bloom (HAB) species, their broad geographic distribution, and the breadth of their impact on different ecosystem components create complex resource management issues that often require complex, integrative approaches to address them. Ecological forecasts are one type of integrative HAB research product that can assist coastal managers in better managing our resources. Forecasting models can assess HAB probability or project HAB movement (which can affect beach or shellfish closures), or they can be used to identify bloom sources (e.g., seed beds, eddies), "bloom triggers" (e.g., nutrients, water stratification), factors contributing to bloom decline (e.g., predation, water mixing), or factors that control bloom toxicity (e.g., cell density, environmental cues, toxin transfer through the food chain). The most complex HAB forecasting models are built from fundamental knowledge of biological, chemical, and physical dynamics in specific ecosystems and depend upon integration of that knowledge with data from various sources, which can include satellite imagery, monitoring partnerships, and *in situ* observations (CSCOR 2011b). Over 1,400 phytoplankton species have been identified from Chesapeake Bay and its tidal tributaries, including

37 potentially harmful species, many of which produce seasonal blooms. The most prevalent and potentially toxic HAB species include *Alexandrium monilatum*, *Cochlodinium polykrikoides*, *Microcystis aeruginosa*, *Prorocentrum minimum*, and *Karlodinium veneficum*. Blooms of these species may impact regional finfish and shellfish populations and degrade water quality conditions in addition to affecting water based industries and human health (Brown 2010, personal communication).

KEY FINDINGS

The potential risk of HABs to human health, natural resources and environmental quality has increased the urgency of routinely monitoring the spatial and temporal distribution of HABs and the frequency of their occurrence in order to prepare and respond to their effects in both the short- and long-term. In the summer of 1997, the Pocomoke River, Kings Creek on the Manokin River, and the Chicamacomico River, all tributaries of Chesapeake Bay, experienced toxic outbreaks of *Pfiesteria piscicida*. These outbreaks led to the implementation of a comprehensive monitoring and research effort by the State of Maryland and its partners to evaluate the factors that are associated with outbreaks of *P. piscicida* and related species with potential toxicity and to provide fish and water quality data needed to fulfill MD DNR's mission. This monitoring effort has expanded over the years to include all potentially toxic or harmful algal species that impact aquatic health and/or human health. Information on HABs is also needed for assessing a regulatory water quality standard for the State of Virginia.

State agencies require regular and accurate short-term predictions (nowcasts of existing conditions to 3-day forecasts) of HAB events and water quality conditions associated with these events to protect fisheries and human health and to direct sampling of toxin and precursor indicators in potential bloom areas, as well as to meet statutory requirements to assess the presence of HABs. Routine measurements of numerous physical, chemical, and biological variables in the Bay must also be acquired or derived to initialize the forecast models and validate the generated predictions. These measurements must include all input parameters required to run the models, such as atmospheric temperature and river flow, as well as those variables predicted and used in HAB forecasts and by management, e.g., the abundance of the target HAB species, to estimate the accuracy of the predictions or skill scores.

Maryland and Virginia have monitored phyto-

plankton composition and abundance, including HAB species, for the past two decades within Chesapeake Bay and its tidal tributaries. These measurements are accompanied by the collection of water quality variables, such as temperature and nutrient concentrations. In Maryland, routine phytoplankton samples are collected 12 times a year at 13 sites by Morgan State and included in the Chesapeake Bay Program database. A similar routine monitoring program is conducted in Virginia by Old Dominion University (ODU). In addition, the Maryland Department of the Environment (MDE) and Maryland Department of Natural Resources (MD DNR) and the Virginia Department of Environmental Quality (VA DEQ), Department of Health (VDH), Virginia Institute of Marine Science (VIMS), and ODU all coordinate response monitoring of HABs in their respective areas to calls from concerned citizens, follow ups from fish kills, and tracking a potentially harmful bloom found during routine monitoring.

This long monitoring time series has advanced the development a prototype system and continued monitoring data is critical to ground truth forecasting models. Unfortunately, difficult economic times at the state level has forced Maryland to eliminate much of its standard phytoplankton monitoring and reprioritization within the Chesapeake Bay Program has raised the possibility of limiting or eliminating standard phytoplankton monitoring in Maryland and Virginia waters of Chesapeake Bay. Forecast models of harmful algae blooms, as a consequence, are needed more than ever to guide the use of potentially limited monitoring resources and direct sampling of bloom events. A prototype Chesapeake Bay HAB prediction system described herein exists that currently generates daily nowcasts and 3-day forecasts of the relative abundance of *Karlodinium veneficum* and the probability of blooms of the HAB species *Prorocentrum minimum*, and *Microcystis aeruginosa* in Chesapeake Bay and its tidal tributaries. The present system uses real-time and 3-day forecast data acquired 3-dimensional coastal models to drive multi-variate empirical habitat models that predict the probability of blooms caused by these HAB species. In the future, the system may incorporate satellite measurements and *in situ* observations. The predictions, presently computed on a server at the NOAA Chesapeake Bay Office and presented as digital images, are available on a web site http://155.206.18.162/cbay_hab/ to individuals and interested agencies to guide research, recreational and management activities. Once the predictions of bloom probability for the three HAB species

are initially available, they will be considered experimental until the approach and predictions are transitioned to operations.

A separate project generates seasonal forecasts of the distribution and intensity of *P. minimum* and *M. aeruginosa* have been generated within the Maryland region of the Bay using similar empirical methods by EcoCheck, a NOAA - UMCES partnership (<http://www.eco-check.org/forecast/chesapeake/2009/>) since 2006. For example, the severity of *Microcystis* blooms in the Potomac River is based on a linear relationship between total Potomac River flow and the percent of water quality samples containing bloom levels of *Microcystis* (Brown *et al.* 2010).

CONCLUSIONS

The demonstration Chesapeake Bay Regional Ocean Modeling System (ChesROMS) hydrodynamic model continues to daily generate nowcasts and 3-day forecasts of the relative abundance of *Karlodinium veneficum* and the likelihood of blooms of *P. minimum* and *M. aeruginosa* in the Bay. All components of the infrastructure to generate, display, and distribute the HAB predictions are consequently under “one roof” at the NOAA Chesapeake Bay Office, alleviating many of the troubles associated with previously distributed constructs of the HAB prediction system. This version of ChesROMS provides predictions of physical properties (temperature and salinity) for driving the HAB, sea nettle and *Vibrio spp.* predictions. The retrospective version of ChesROMS is currently available to the public (Figure 9).

Much effort over the past year has focused on continued “tuning” and debugging of the biogeochemical model in the Regional Ocean Modeling System (ROMS) for Chesapeake Bay in order to predict relevant water quality variables, such as chlorophyll, and nitrate concentration, necessary to drive the habitat suitability models of the target HAB species. Though validation of the biogeochemical fields continues, the biogeochemical model has been successfully implemented into the operational version of ChesROMS and is routinely generating preliminary forecasts of several water quality variables of the Bay that are displayed on an initial web site (http://155.206.18.162/chesroms_ecocast/).

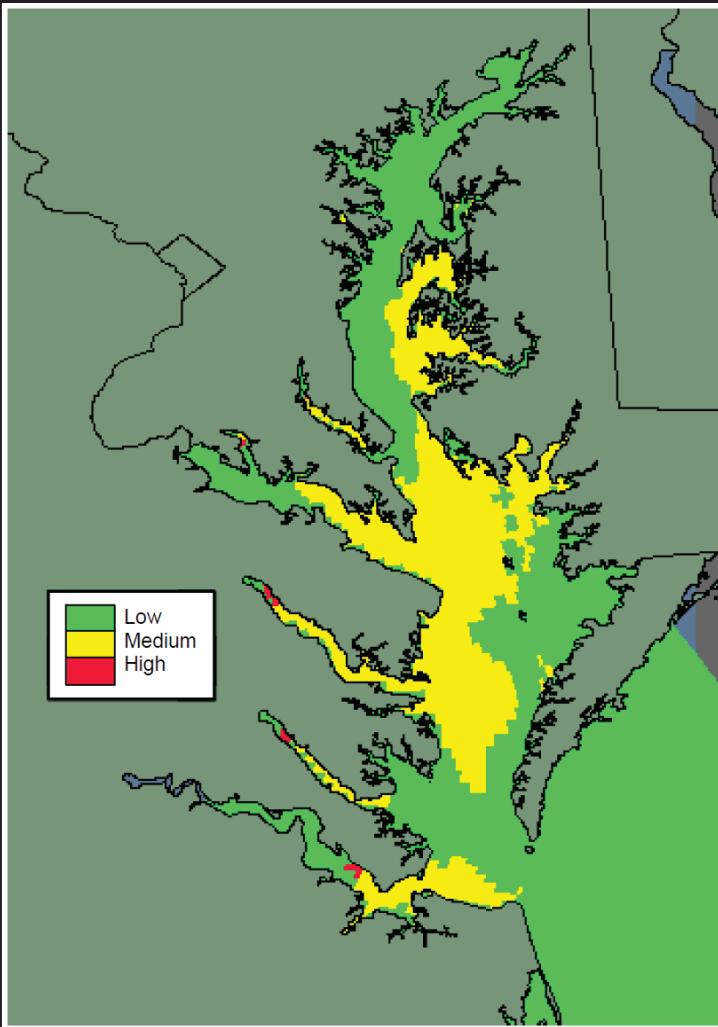
In anticipation of assimilating satellite-derived sea-surface temperature (SST) into the prediction system, the project continues to evaluate how well they compared against SST derived from using the operational ChesROMS database. The project continues

analysis to better understand the discrepancy between satellite- and model-derived SSTs before incorporating the satellite SSTs into the prediction system.

Maryland DNR continues to collect and maintain oversight of data collection, QA/QC, storage, and online dissemination of the water quality and phytoplankton data totaling > 10 million data points per year. DNR also works to combine all the plankton data into a single Access database. These data are being used in evaluating model development and are being used in the habitat model development component and verification process of the project. Maryland DNR continues to run a web-based, map interface to display current densities of the three species of concern. The map displays results of samples collected in the two-week period preceding posting. Maps are updated weekly and can be viewed at: http://mddnr.chesapeakebay.net/hab/HAB_maps.cfm (Brown 2010, personal communication).

PLANNED AND POTENTIAL ECOLOGICAL

Figure 9. Relative Abundance of *Karlodinium veneficum* - 03/18/2011 Chesapeake Bay HAB Forecasts web site, http://155.206.18.162/cbay_hab/index.php



FORECASTING IN CHESAPEAKE BAY: LOOKING TO THE FUTURE

A number of NCCOS and NCCOS-sponsored projects are under development, planned, or being expanded relating to ecological forecasting in Chesapeake Bay. Many of these projects are in partnership with other NOAA offices and state agencies. These activities include operational forecasting of pathogens, sea nettles, hypoxia and HABs (Hood *et al.* 2010, Aikman *et al.* 2010 and Figure 10).

Pathogens

In collaboration with the Cooperative Oxford Laboratory, the MERHAB prediction system project has extended its system to predict daily nowcasts and 3-day forecasts of the likelihood of the pathogen *Vibrio vulnificus* in Chesapeake Bay. A new web site has been constructed and implemented (<http://155.206.18.162/vvul>) to display the forecasts and a NOAA Technical Memorandum is now available describing the *V. vulnificus* habitat model and model predictions (Jacobs *et al.* 2010, Jacobs *et al.* 2011).

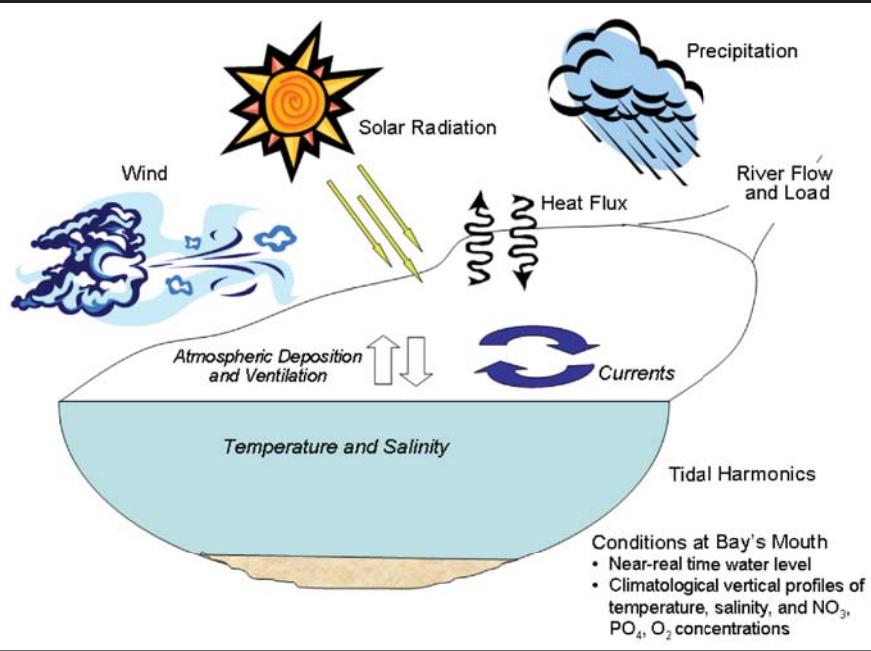
Sea Nettles

Although NCCOS funding ended in FY 2008 for the project to develop an operational model for predicting the near real time distribution and abundance of the sea nettle jellyfish, *Chrysaora quinquecirrha*, the project transition to operations has been picked up by the NOAA National Weather Service (NWS) as part of their expanding effort to move beyond weather forecasts into ecological forecasts. This effort shows how long it can take (going on 6 years) for a project to move into a successful operational mode. This will be the first time that ecological forecasting is incorporated into NWS weather forecasts. Sea nettles forecasts are being used as a prototype with the bacterium *Vibrio* also being considered next for prediction (Decker 2008).

Hypoxia

In 2007 CSCOR began a sponsored Chesapeake Bay study to model hypoxia and ecological responses to climate change and nutrients. This project, building on earlier research and funded under the Coastal Hypoxia Research Program (CHRP), is developing science-based forecasting tools readily implemented for any coastal system to simulate ecological responses to climate and nutrient management. The project combines: retrospective analysis of existing data, diagnostic assessment of mechanisms underlying observed ecological systems,

Figure 10. Schematic of the Chesapeake Bay Regional Ocean Modeling System (ChesROMS). ChesROMS simulates salinity, temperature, and other physical variables in the bay (Aikman *et al.* 2010).



simulation studies that develop numerical models to forecast and analyze water quality responses to climate and nutrient management, and evaluation of the size and quality habitats for selected fish and invertebrate populations. Model simulations will include routine seasonal forecasts of hypoxia distributions and intensity in summer seasons based on spring climatic and ecological conditions and on average summer climatology (CSCOR 2011d). Hypoxia research in CSCOR is authorized by the Harmful Algal Bloom and Hypoxia Research Control Act (HABHRCA) of 2004.

Harmful Algal Blooms (HABs)

As described earlier, the prototype Chesapeake Bay HAB prediction system developed by NOAA, the University of Maryland Center for Environmental Science (UMCES), and MD DNR currently generates daily nowcasts and 3-day forecasts of the relative abundance of *Karlodinium veneficum*. For the future, it will generate daily nowcasts and 3-day forecasts of the probability of blooms of the HAB species *K. veneficum*, *Prorocentrum minimum*, and *Microcystis aeruginosa* in Chesapeake Bay and its tidal tributaries, where a bloom is operationally defined by MD DNR as 10,000 cells/ml for *K. veneficum* and 3,000 cells/ml for *P. minimum*, and 10,000 cells/ml for *M. aeruginosa*, the first threshold in a gradient of bloom concentrations related to human health risks of these cyanophyte blooms. The system presently uses real-time and 3-day forecast data acquired from a 3-dimensional coastal models, to drive a

multi-variate empirical habitat model that predicts the probability of blooms caused by these HAB species. The empirical habitat models relate ambient environmental conditions to the probability or abundance of the target species. This hybrid empirical-mechanistic approach was adopted because mechanistic models cannot be presently constructed due to our limited understanding of the factors initiating blooms of most HAB species. The predictions, presently computed on a server at the NOAA Chesapeake Bay Office and presented as digital images, are available on a web site (http://155.206.18.162/cbay_hab/) to individuals and interested agencies to guide research, recreational and management activities. The predictions for the three HAB species are considered experimental until the approach

and predictions are transitioned to operations (Brown *et al.* 2010).

Transition of the HAB predictions to operations will require the routine collection and availability of in-situ observations and remote measurements to regularly initiate the numerical models, assess the skill of their predictions, and improve their forecasts. This capability will require the development of new observational capabilities, ranging from the creation of new sensors that can identify individual HAB species to the use of measurements from multiple sampling platforms, such as ships, buoys, automated underwater vehicles (AUVs), and satellites (Aikman 2010).

A network must also be established in order to distribute both HAB and HAB-related data and predictions to users and stakeholders in a timely fashion. The Mid-Atlantic Coastal Ocean Observing Regional Association (MACOORA), in concert with its member, the Chesapeake Bay Observing System (CBOS), and its primary funding source, the Integrated Ocean Observing System (IOOS), recognizes the need for observations in the Chesapeake Bay system in order to support wise decision-making and appropriate management solutions. A number of observing platforms are currently in place, and include the NOAA Chesapeake Bay Interpretive Buoy System (<http://www.buoybay.org/site/public/>), the Maryland DNR's Eyes on the Bay (www.eyesonthebay.net) and the Virginia Estuarine & Coastal Observing System (VECOS) (<http://www2.vims.edu/vecos>), but a greater integration between these existing

observing systems and future ones is essential to support and maintain an operational HAB forecast system in Chesapeake Bay. Lastly, the operational HAB prediction system will require funding for its operation, maintenance, and incremental enhancements (Brown *et al.* 2010).

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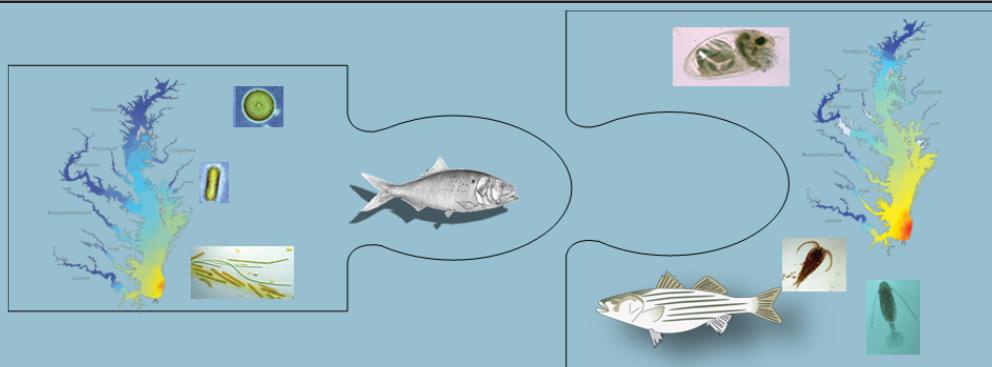
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CHAPTER 3:

Impacts of Climate Change and Variability on Fish Production in Chesapeake Bay and the Mid-Atlantic Coast



R.J. Wood^{1*}, E.J. Martino¹, J. Johnson², and X. Zhang¹.

National Centers for Coastal Ocean Science,

Center for Coastal Environmental Health and Biomolecular Research, Cooperative Oxford Laboratory¹

USEPA Chesapeake Bay Program Office, Interstate Commission on the Potomac River Basin²

*Corresponding author, bob.wood@noaa.gov, 410-226-5193 (phone), 410-226-5925 (fax)

INTRODUCTION

The study of environmental processes linked to pronounced variations in coastal and marine fisheries production has significantly enhanced our understanding of climate variability effects on ecosystem form and function. Information on climate-driven ecosystem variability supports recent ecosystem-based fishery management efforts for “adapting fishing pressure to environmental conditions and food-web interactions” (Lindgren, 2009). A better understanding of how climate variability and large scale climate patterns affect the world’s coastal ecosystems also provides insight into possible effects of future climate changes on ecosystem services provided by these highly dynamic systems. A recent interdecadal multispecies fish recruitment pattern was detected in Chesapeake Bay, USA, one of the largest estuarine ecosystems in the world (Wood and Austin, 2009). This pattern describes a strong negative relationship between recruitments of estuarine-dependant anadromous and shelf-spawning fishes (CBASS, Figure 1). This finding has important implications both for the Chesapeake ecosystem and the larger Northeast United States Continental Shelf

Large Marine Ecosystem (NEUCS-LME) because Chesapeake Bay serves as a critically important production and feeding ground for economically and ecologically important coastal Atlantic fish populations. Anadromous striped bass (*Morone saxatilis*) and estuarine dependant shelf-spawning Atlantic menhaden (*Brevoortia*

Figure 1. Scatterplot matrix comparing annual mean young-of-the-year abundance (log transformed) for anadromous and coastal spawning estuarine-dependent fish species. Data from the Maryland Department of Natural Resources juvenile fish seine survey. Correlation among all species pairs is significant ($p \leq 0.05$), with the exception of that between alewife and spot.

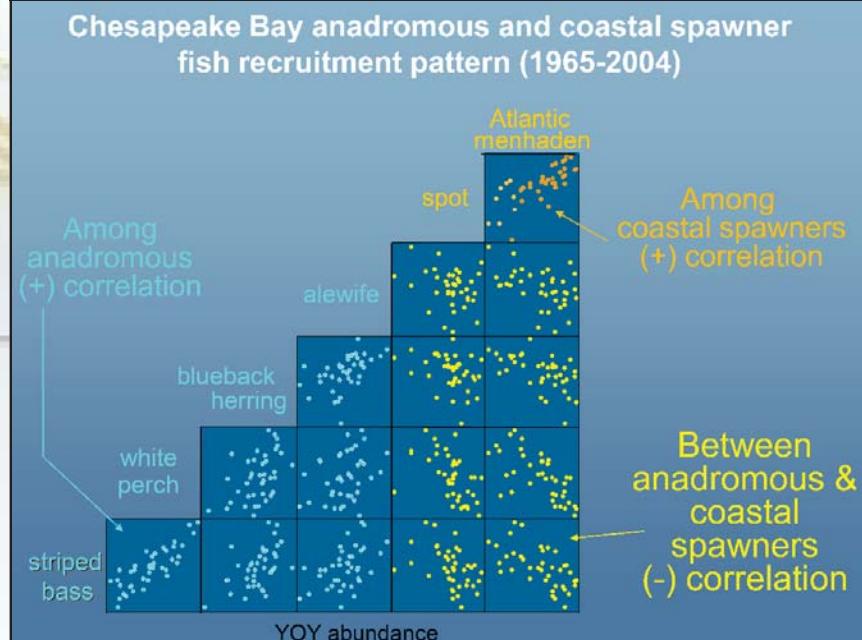
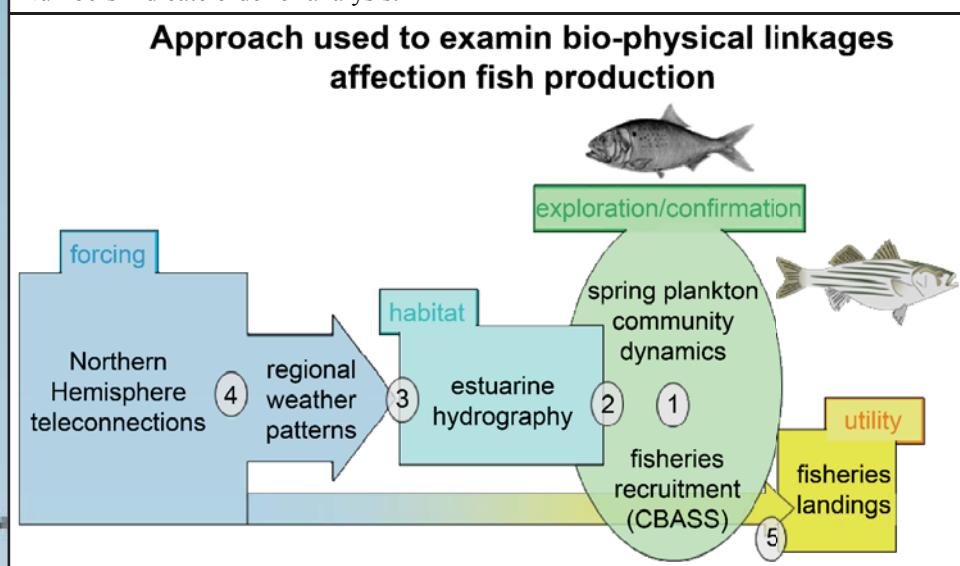


Figure 2. Conceptual diagram of the methodological framework employed in this study. Numbers indicate order of analysis.



tyrannus) are two species whose interannual recruitment dynamics are well described by the CBASS pattern. These two species support valuable commercial and recreational fisheries, and they also play key ecological roles as coastal migratory predators and filter-feeding foragers (respectively), in coastal Atlantic waters and estuaries from North Carolina to the Canadian Maritime provinces.

Mechanism underlying the inverse CBASS-recruitment pattern are unknown but are likely controlled by broad scale climate-driven environmental variability (Wood and Austin, 2009). In this study we examined Chesapeake Bay plankton community dynamics, hydrography, and regional and larger-scale climate patterns to provide insights that can support development of more effective fisheries management policies (Figure 2).

RESULTS

Chesapeake's springtime plankton community and fish recruitment

We used principal component analysis (PCA) to define a pattern in oligo-mesohaline transition zone (OMTZ) annual plankton abundance represented here as plankton principal component 1 (PPC1). The community dynamics represented by PPC1 is defined by a negative relationship between the abundance of dominant early-spring phytoplankton taxa and mid-to-late spring zooplankton taxa.

PPC1 reveals a negative relationship between taxa that are known to be important prey for young-of-the-year Atlantic menhaden and larval-to juvenile-stage striped bass. These findings suggest that the CBASS pattern may be driven by prey availability, but physical dynamics within the OMTZ could be coincidentally influencing both the plankton community and fish production patterns. In either case, the findings suggest that climate dynamics are driving estuarine hydrography and controlling inter-annual variability in the CBASS pattern.

Weather, hydrography, fish production, and plankton

PPC1 was found to be strongly correlated with the CBASS (Figure 3, $r=0.75$, $p=0.0006$). PPC1 and the CBASS were each found to be significantly correlated with cumulative precipitation over the northern Chesapeake watershed and salinity within the OMTZ (Figure 4). While atmospheric temperature was moderately correlated with both PPC1 and the CBASS (for each, $p\leq 0.1$), spring water temperature was not. These findings reveal conspicuous contrasts in Chesapeake Bay hydrographic structure and associated biological effects in wet versus dry years (Figure 5). Strong negative correlations between precipitation and both PPC1 and CBASS time series were found to occur over a region that includes the Chesapeake Bay watershed and

Figure 3. Time series of salinity, freshwater flow, fish recruitment (CBASS), and plankton (PPC1) for the years 1985-2001.

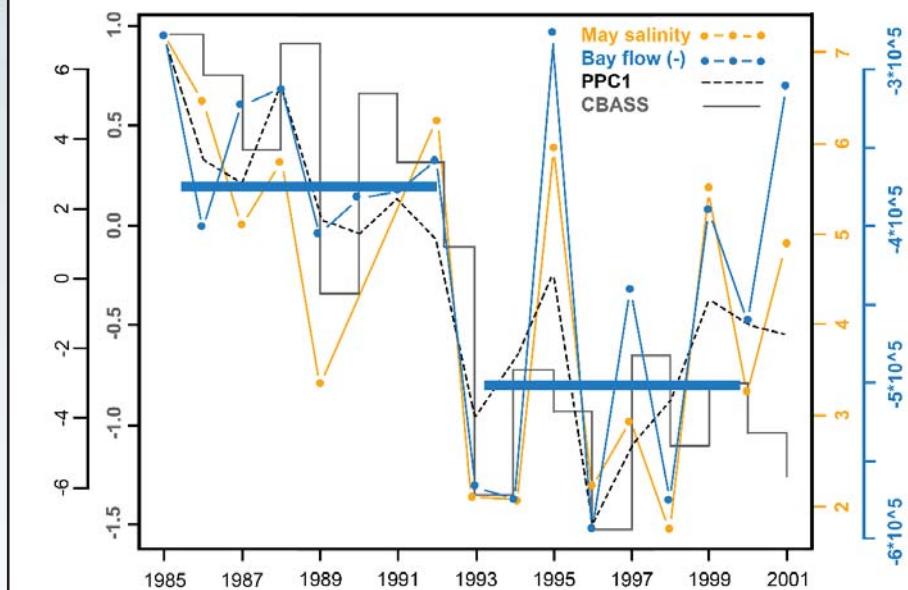


Figure 4. Top row: Correlation between December-June mean precipitation for each continental U.S. climate division and A) PPC1 and B) CBASS. Bottom row: Correlation between March-June mean surface air temperature for each continental U.S. climate division and C) CBASS and D) PPC1.

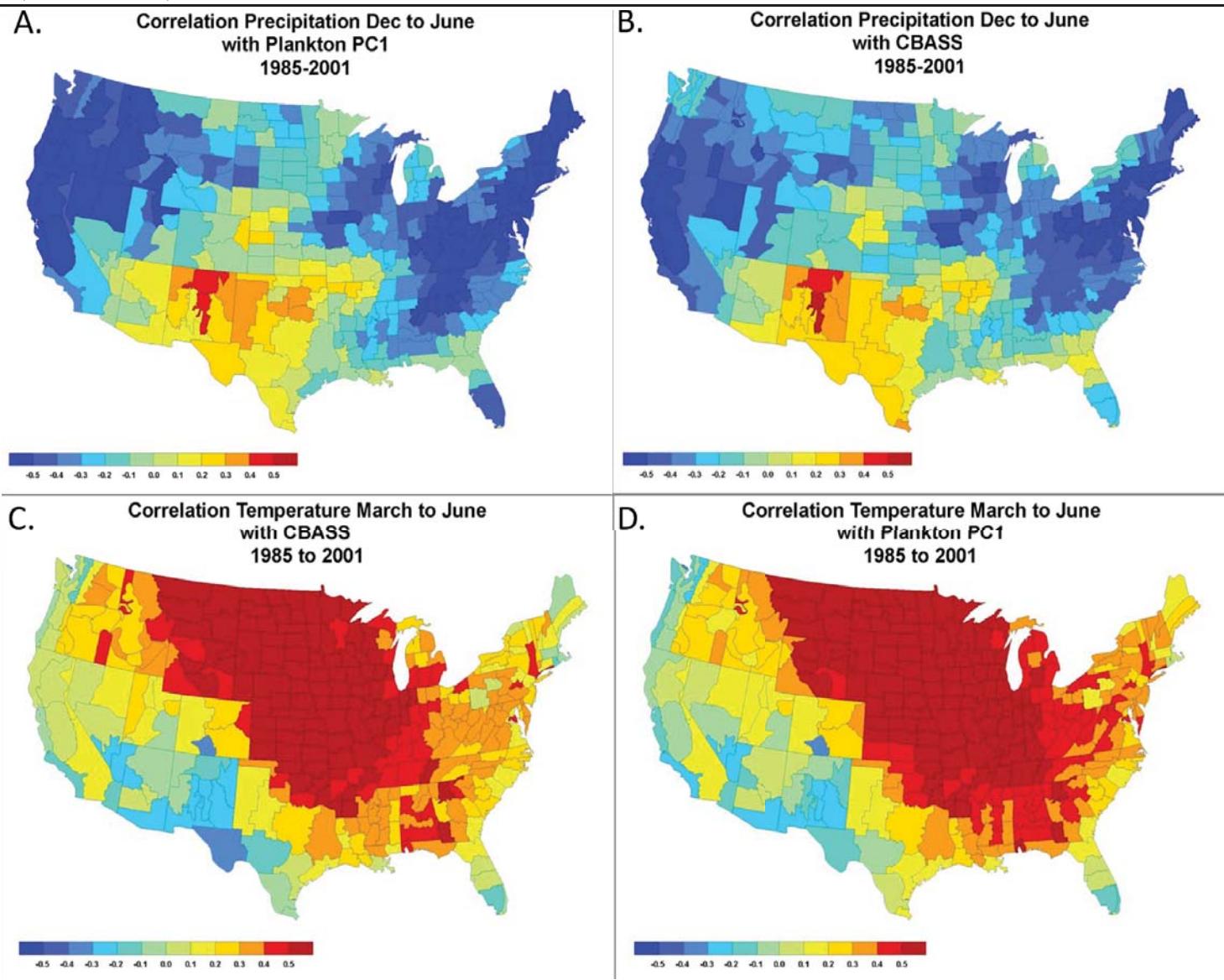
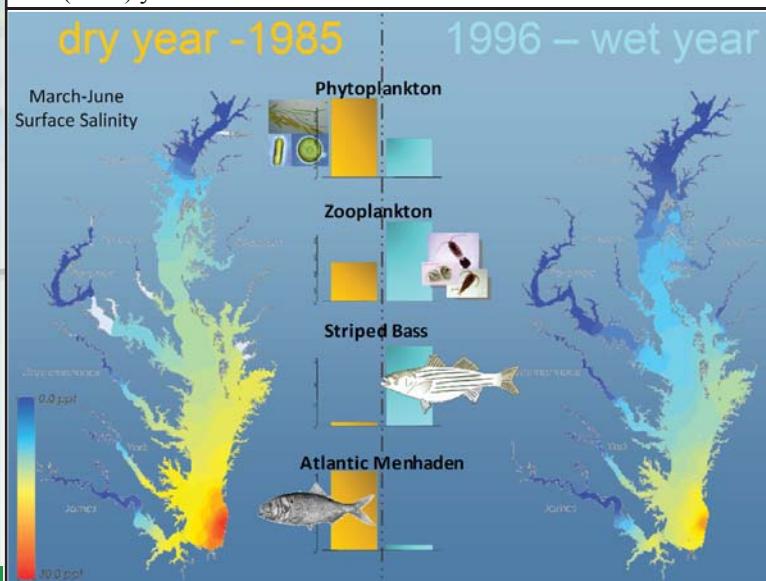


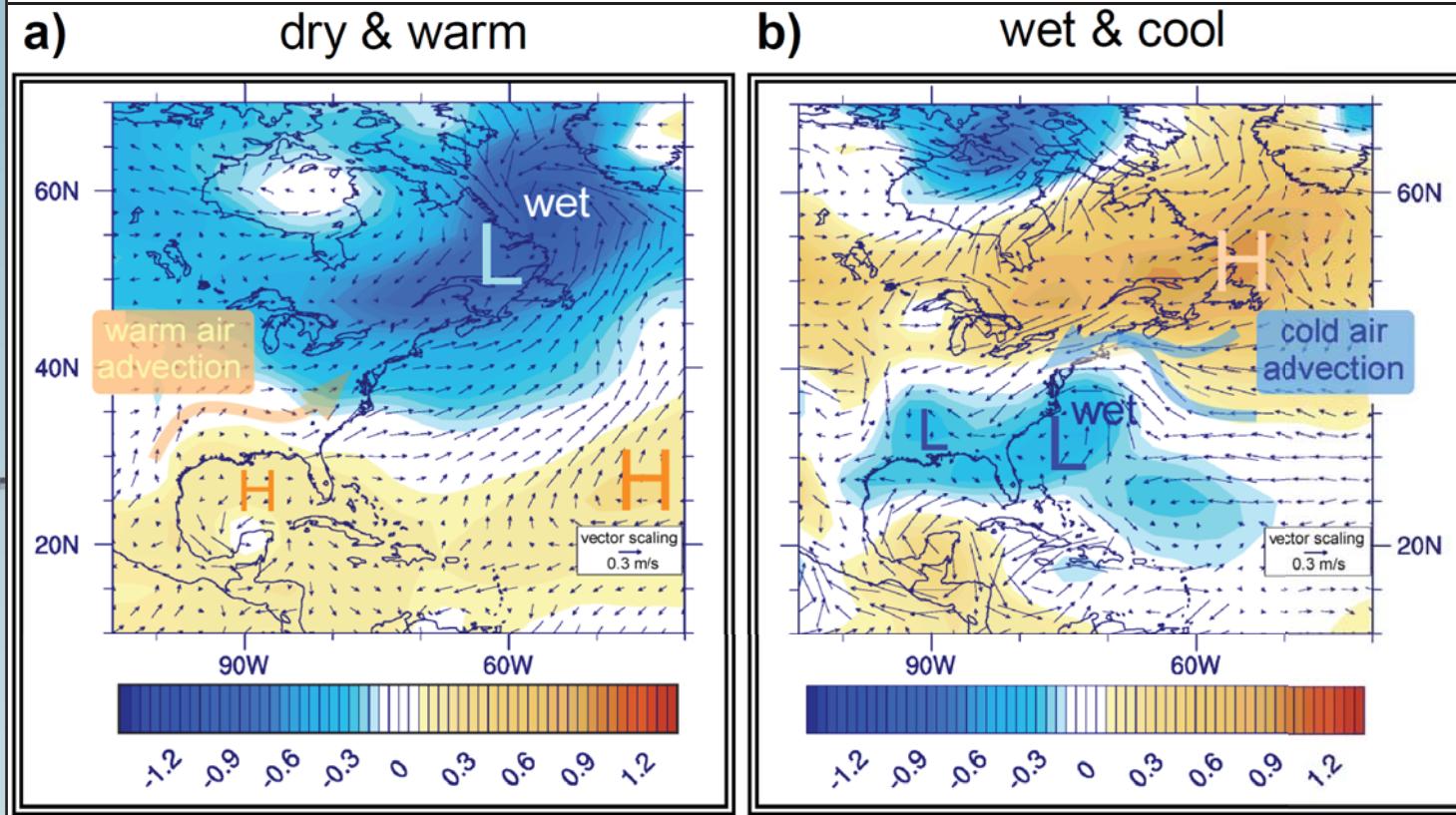
Figure 5. Distribution of Chesapeake Bay salinity, and the abundance of plankton, striped bass, and Atlantic menhaden in a dry (1985) and wet (1996) year.



also portions of the Appalachian Mountains, the Ohio River valley, and New England. However, while strong (positive) temperature correlations with both series occur over much of the central US, temperature correlations across the Chesapeake watershed were relatively weak.

The weather correlations are consistent with antagonistic sea level pressure (SLP) and surface wind anomalies that occur across central and eastern North American in years associated with high production of menhaden (Figure 6a) and striped bass (Figure 6b). When Atlantic menhaden production is strong (favoring + CBASS) positive SLP anomalies occur below 30°N latitude, while negative SLP anomalies occur above 40°N, with a conspicuously strong negative low pressure anomaly residing over the Labrador Sea. The pressure

Figure 6. Maps comparing: winter-spring SLP and wind vector anomalies associated with the strongest Chesapeake Bay annual recruitments for a) Atlantic menhaden and b) striped bass. Groupings included years when MDDNR juvenile abundance indices were >75 th percentile, 1966-2009, for each species.



gradients set up by these SLP patterns drive a south-southwesterly (warm) wind stream anomaly that begins in northwestern Mexico and stretches across much of the central and eastern US. In years of strong menhaden production, relatively warm and dry continental southwesterlies are driven by stronger than normal low pressure to the northeast, and a high pressure anomaly to the southwest of the Chesapeake (Figure 6a). In contrast, the pressure gradient established in very strong striped bass years is reversed, reversing the wind field so that winds from the Atlantic Ocean and Canadian Maritimes are advected from the east and northeast, respectively.

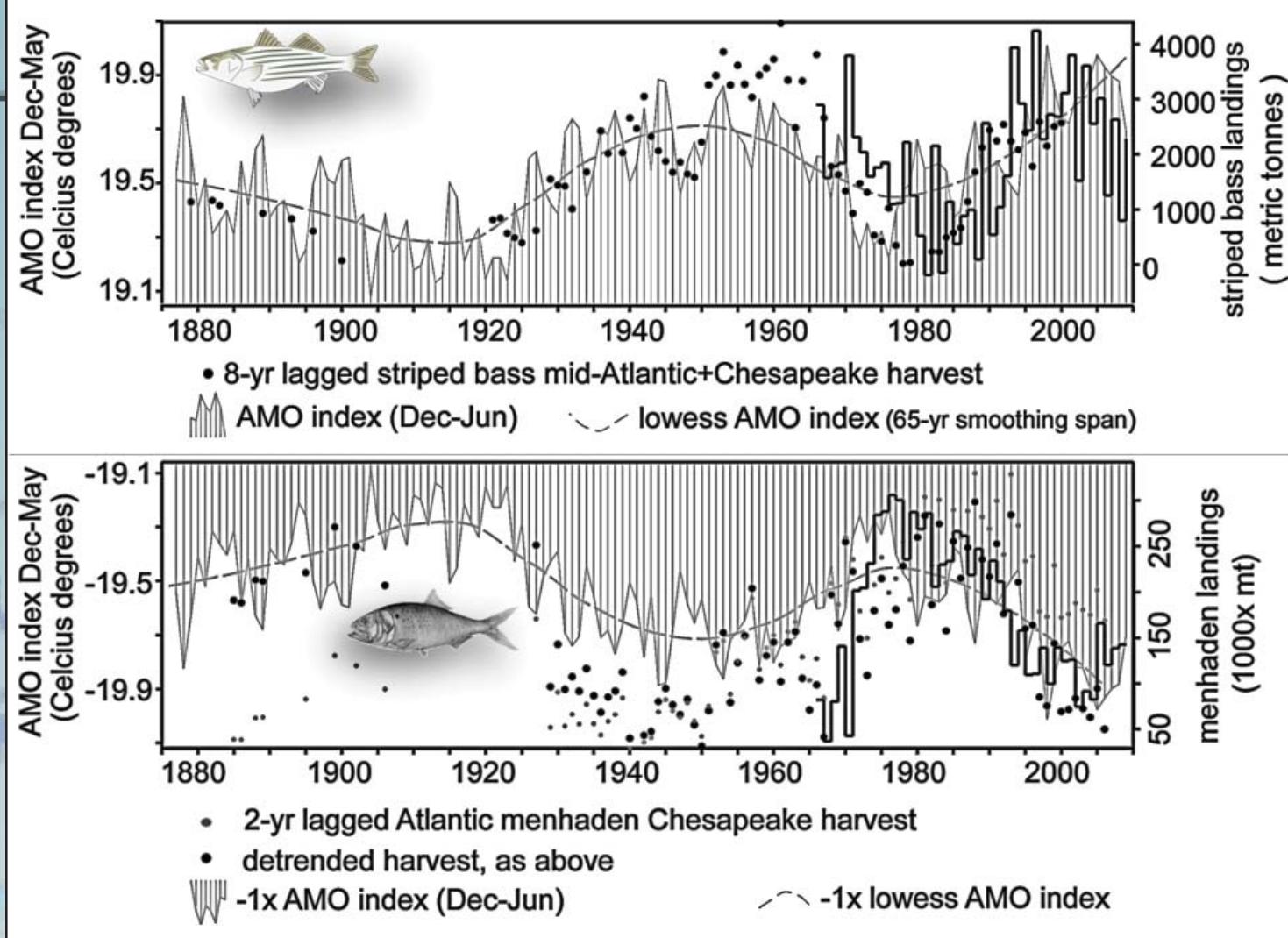
In years when striped bass recruitment is strongest, positive SLP anomalies stretch across southern Canada and the northern US, with the strongest positive values residing above the Canadian Maritimes and the southern Labrador Sea (mirroring the strong low there during strong menhaden production years), while a low pressure anomaly stretches across the Gulf coast to Cape Hatteras. The low pressure band anomalies associated with strong striped bass production years includes the primary cyclogenesis regions for US east coast winter storms (Mather *et al.*, 1964; Whittaker and Horn, 1981; Davis *et al.*, 1993). Accordingly, the production of striped bass was compared to, and found to

be significantly correlated with ($r=0.38$, $p=0.0075$), the number of annual East Coast Winters Storms affecting the mid-Atlantic and Northeastern US. Further, as the pressure gradient set up by these SLP patterns is opposite those occurring in strong menhaden production years, they result in northeasterly wind anomalies that stretch from the Canadian Maritimes across much of the eastern and central US including the Chesapeake watershed, the Great lakes region, and the Gulf coast states.

Teleconnections, fish recruitment, and fishery landings

The Atlantic Multidecadal Oscillation (AMO) was strongly correlated with the CBASS, and the AMO index averaged over December to June (-0.51 , $p<0.001$) was more strongly correlated than that for March-June (-0.43 , $p\leq0.005$) (Figure 7). The winter-spring AMO, features a pronounced sinusoidal wave component over the last century. Lowess smoothing (60-year smoothing span) of the AMO winter-spring index yielded a sinusoidal wave pattern accounting for 78% of the series' total variance over the last century (Figure 7). While lagged striped bass landings were significantly correlated with both the raw and lowess-smoothed AMO series, the lagged Atlantic menhaden landings were significantly correlated only after detrending.

Figure 7. The relationship between the December to May AMO index (gray lines), and both landings (black dots) and log10 juvenile recruitments (black lines) for a) striped bass and b) Atlantic menhaden. Landings were lagged according to the average age of Atlantic menhaden landed in the Chesapeake fishery (2 years old) and of striped bass (8 years) landed in the coastal fishery as specified by ASMFC.



CONCLUSION

The findings reported here enhance our understanding of climate-ecosystem interactions affecting Chesapeake Bay and larger NEUCS-LME, and provide needed insight on possible effects of future climate change. Results of this investigation have established that variability in Chesapeake Bay fish production, as described by the CBASS recruitment pattern, is strongly associated with synchronous fluctuations in the estuary's plankton dynamics. Further, changes in fish and plankton are associated with variability in hydrographic structure, and with climate patterns that operate over broad spatial and temporal scales. The findings reported here may provide resource managers with information on future resource availability in advance of projected changes in the AMO. Relationships identified in this study provide an opportunity to inform

new strategic, forward-looking policies that consider climate-driven cyclical changes in Chesapeake Bay fish production.

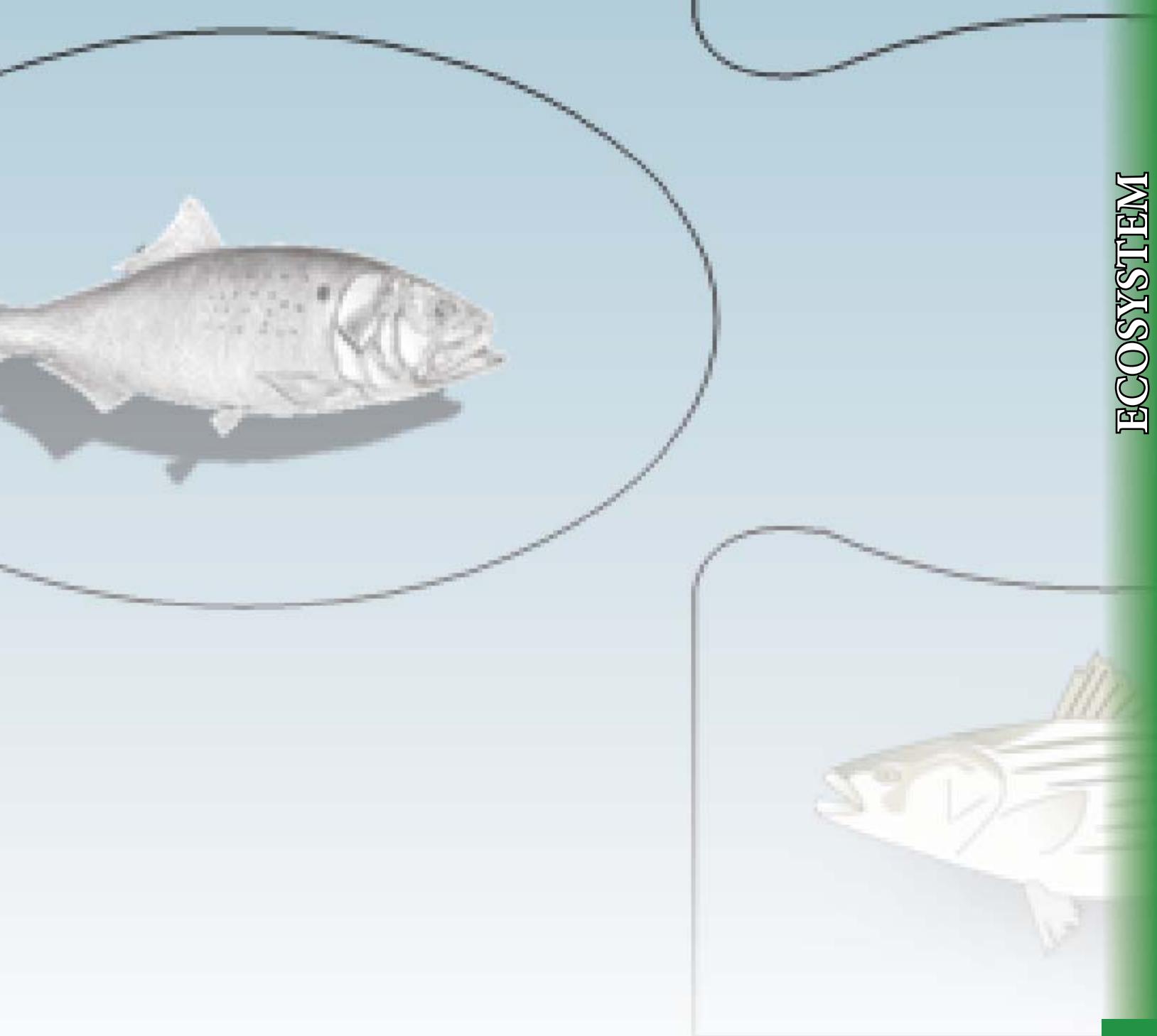
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CHAPTER 4:

Eutrophication Assessment in Chesapeake Bay and Tributaries



Suzanne Bricker*

National Centers for Coastal Ocean Science,
Center for Coastal Monitoring and Assessment

*Corresponding author, suzanne.bricker@noaa.gov, 301-713-3020, x139 (phone), 301-713-4384 (fax)

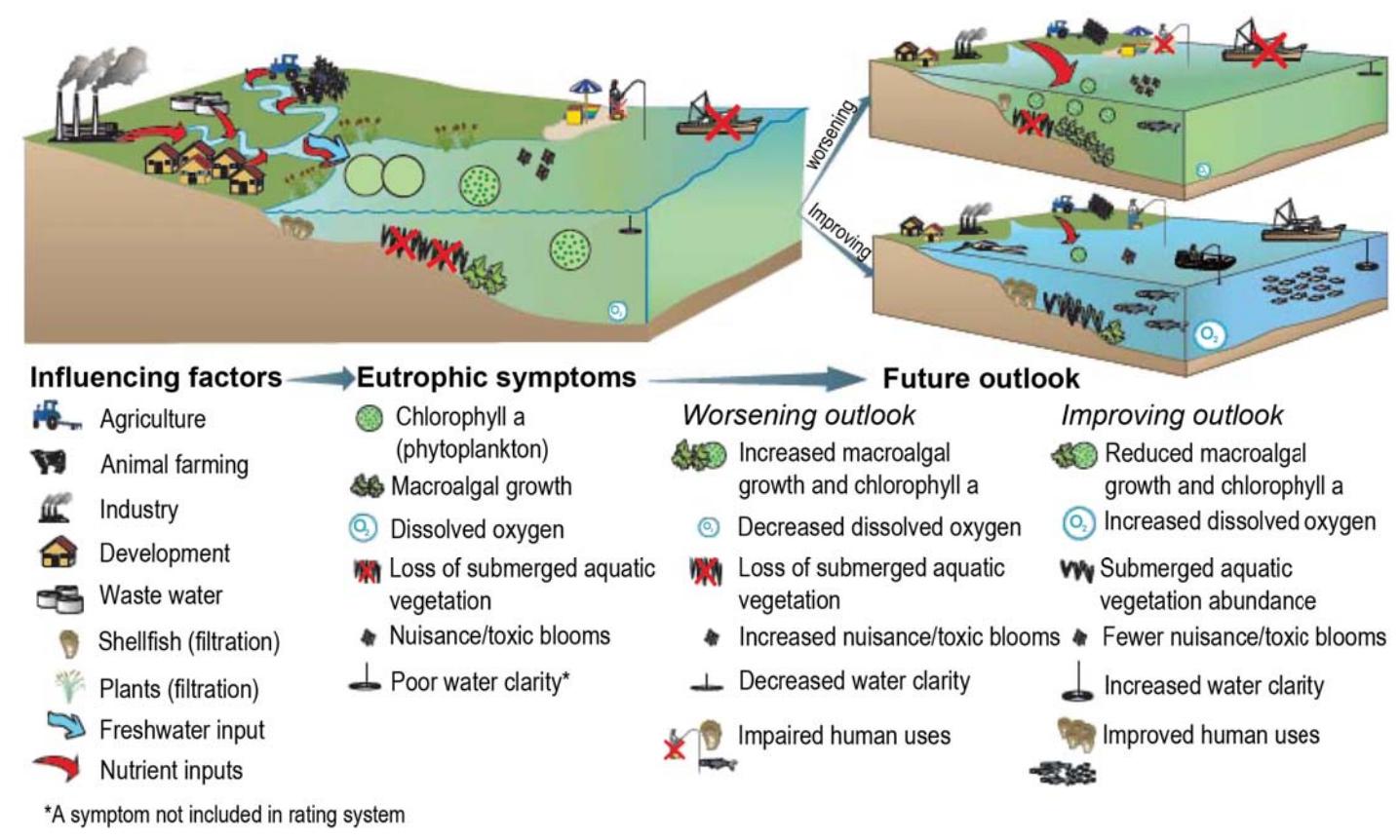
KEY FINDINGS

- Eutrophication, or nutrient pollution, causes excessive algal growth which can cause other problems such as low dissolved oxygen and dieoff of seagrasses.
- Eutrophication is a widespread problem, with 65% of systems assessed in the National Estuarine Eutrophication Assessment, representing 78% of assessed estuarine area within the US coastal zone exhibiting moderate to high eutrophic conditions.
- The mid-Atlantic Region, where the Chesapeake Bay and tributaries are located, is the most highly impacted region in the US; the Chesapeake estuaries are among those with the worst conditions in the region.
- The major impacts are high levels of algal growth shown by high chlorophyll a concentrations, problems with nuisance and toxic algal blooms and problems with low dissolved oxygen in bottom waters.
- Causes of nutrient related impairment in the Chesapeake systems are nutrient loads from wastewater treatment plants, crop and animal agriculture and urban runoff.
- Living resources are impaired by nutrients and in the Chesapeake estuaries there are noted impairments to shellfish, commercial and recreational fishing and fish consumption.
- In Patuxent and Potomac River estuaries the expected catch of striped bass is shown to increase when dissolved oxygen concentrations increase, suggesting that eutrophication impacts human-uses in a negative way.
- One third of Chesapeake Bay estuaries are expected to exhibit worse conditions in the future while one third are expected to improve.

What is Eutrophication?

Eutrophication refers to a process in which the addition of nutrients to water bodies, primarily nitrogen and phosphorus, stimulates algal growth. This is a natural process; estuaries have always received nutrients from natural sources from weathering of the watershed and from the ocean through tidal exchange. In recent decades, however, population growth and related activities, such as various agricultural practices, wastewater treatment plants, urban runoff, and the burning of fossil fuels have increased nutrient inputs by many times the levels that occur naturally.

Figure 1. Eutrophication assessment components and impacts.



Increased nutrient inputs promote a complex array of symptoms, beginning with the excessive growth of algae, which in turn may lead to more serious symptoms such as low dissolved oxygen, losses of seagrasses, fish kills and loss of fish diversity (Figure 1). In addition to the rate of algal growth, nutrient inputs may also affect which algal species are favored. This process is poorly understood, but some unfavorable species that

are toxic or a nuisance (e.g., *Pfiesteria*) appear to be linked to nutrient inputs. In some estuaries, nutrients cause dense algal blooms to occur for months at a time, blocking sunlight to submerged aquatic vegetation. Decaying algae from the blooms uses oxygen that was once available to fish and shellfish. In other estuaries, these or other symptoms may occur, but less frequently, for shorter periods of time, or over smaller spatial areas. In

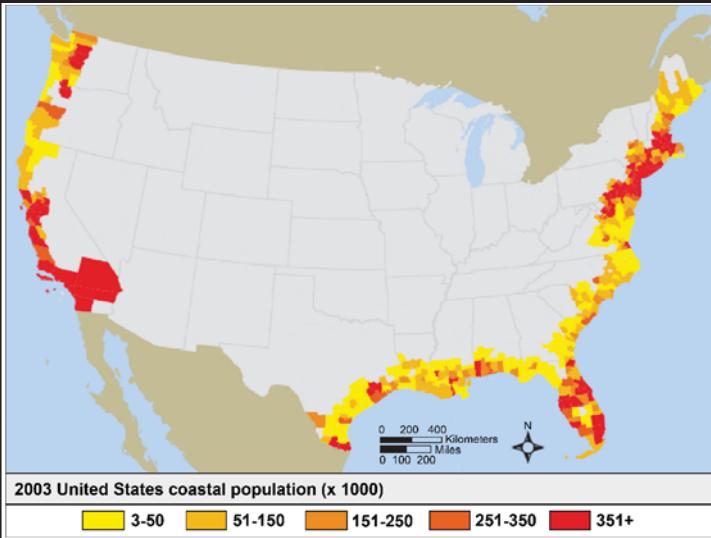
Table 1. Summary of physical characteristics for each region and within regions nationally*

Region	Estuarine area (km ²)	Depth (m)	Tidal height (m)	Watershed area (km ²)	Watershed elevation (m)	Annual precipitation (m)	Annual temperature (°C)	Frost days (days)
North Atlantic	264	12.9	2.8	4,284	100	1.16	8	156
mid-Atlantic	923	4.7	0.8	13,521	116	1.12	13	106
estuaries	1,140	5.7	0.86	17,137	147	--	--	--
lagoons	189	1.4	0.59	1,232	12.6	--	--	--
South Atlantic	534	2.9	1.21	15,043	58	1.32	19	36
NC to GA	522	3.2	1.32	15,678	56	1.31	19	41
Florida	761	1.4	0.48	11,018	9	1.33	23	5
Gulf of Mexico**	822	1.7	0.41	109,545	107	1.33	22	12
FL MS LA AL	882	1.8	0.47	133,068	73	1.46	22	13
TX	667	1.6	0.26	46,031	198	0.98	22	9
Pacific	182	14	1.5	25,209	401	1.14	12	57
fjord	438	66	2.4	5,822	477	1.07	10	73
river mouth	133	6.9	1.4	42,039	459	1.71	12	66
lagoons	75	3.5	1.1	1,297	271	0.29	16	23

*Data source: S.V. Smith (2003).

**Does not include Mississippi River to avoid biasing the results due to its extreme watershed size.

Figure 2. US coastal population in 2003.



still other estuaries, the assimilative capacity, or ability to absorb nutrients, may be greatly reduced, though no other symptoms are apparent. These eutrophic symptoms are indicative of degraded water quality conditions that can adversely affect the use of estuarine resources, including commercial and recreational fishing, boating, swimming, and tourism. Eutrophic symptoms may also cause risks to human health, including serious illness and death that result from the consumption of shellfish contaminated with algal toxins, or from direct exposure to waterborne or airborne toxins.

Whether nutrient additions result in degraded water quality depends on the magnitude of the inputs and on natural characteristics that affect estuarine susceptibility to nutrients. The susceptibility or sensitivity to nutrients is influenced by the rate at which freshwater enters the estuary, the depth and volume of the estuary and the extent of tidal action. All of these processes work together to flush and dilute incoming nutrients at different rates. As an example, a shallow estuary with limited exchange with the ocean and only a small fresh-

water input may be more susceptible to development of eutrophication because nutrient rich waters stay within the estuary for a long time which gives the algae time to grow. The opposite is true in estuaries where there is a large freshwater input to a deep system that is well mixed by tides, they are less susceptible.

The National Estuarine Eutrophication Assessment (NEEA):

In the early 1990s NOAA's NCCOS conducted the first National Estuarine Eutrophication Assessment (NEEA) to provide a basis for an appropriate and effective national response to nutrient problems in the nation's estuaries. Although studied for decades, consequences of eutrophication had become more apparent. For example, many coastal waterbodies were suffering worsening episodes of low dissolved oxygen and blooms of nuisance and toxic algae were occurring in areas where they had not previously been observed (e.g., *Pfiesteria*, first identified in estuaries of North Carolina in 1992 was observed in 1997 in tributaries of the Chesapeake Bay). The NEEA included assessment of 141 estuaries from the Atlantic, Gulf of Mexico and Pacific coastlines (Table 1). The first report, describing eutrophic conditions in the nation's estuaries in the early 1990s was released in 1999 and an update, looking at eutrophic conditions in the early 2000s and changes during the ensuing decade, was released in 2007.

NEEA Study Sites:

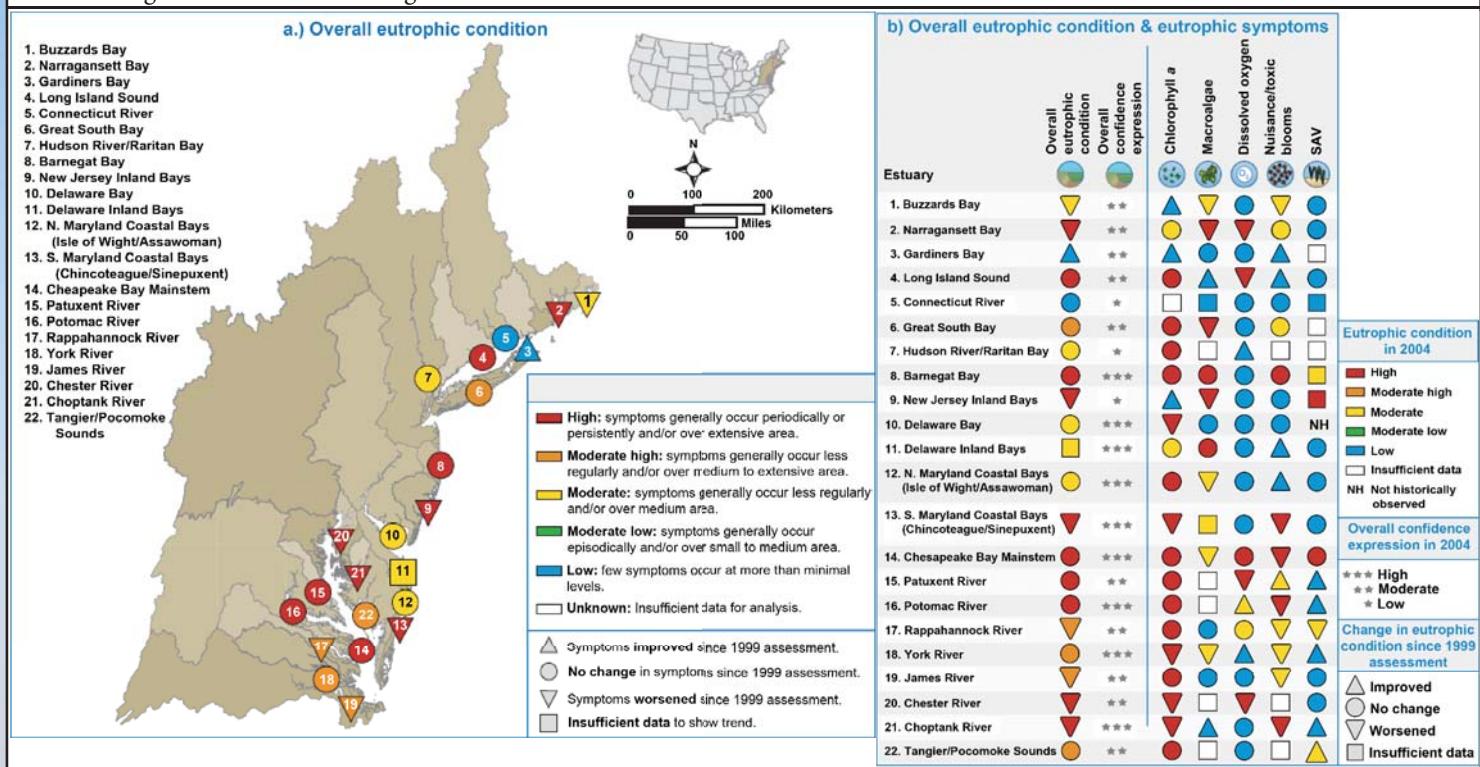
The NEEA divided the US Coastline into regions. The Atlantic coast is comprised of 3 regions, North, Mid and South Atlantic including 10, 22 and 22 estuaries, respectively, The Gulf of Mexico region is comprised of 38 estuaries and the Pacific coast includes 39 estuaries. The Chesapeake Bay, and associated estuaries, is part of the

Table 2. Summary characteristics of Chesapeake estuaries. From: S.V. Smith (2003)

Estuary	Estuarine area (km ²)	Volume (10 ⁶ m ³)	Depth (m)	Tidal height (m)	Average salinity	FW flushing (days)	FW inflow (m ³ s ⁻¹)	Catchment population (10 ³ people)	TN input (ton yr ⁻¹)
Patuxent River	142	537	3.8	0.52	12	26	14	454	1,395
Potomac River	1,260	6,469	5.1	0.55	11	36	395	4,560	20,556
Rappahannock River	377	1,413	3.7	0.53	12	24	51	182	3,081
York River	206	786	3.8	0.82	11	11	47	164	2,829
James River	640	2,062	3.2	0.80	11	8	250	1,802	11,394
Chester River	196	681	3.5	0.48	12	27	1	28	NA
Choptank River	411	1,270	3.1	0.50	13	19	7	50	NA
Tangier/Pocomoke Sounds	1,057	3,479	3.3	0.67	13	12	10	183	7,697
Chesapeake Bay Mainstem	6,974	51,119	7.3	0.45	16	105	1,211	6,409	109,243

FW = Fresh Water; TN = Total Nitrogen

Figure 3. (a) Map of overall eutrophic condition (OEC) and (b) the combination of individual eutrophic symptoms which constitute OEC ratings in the mid-Atlantic region.



mid-Atlantic region and includes estuaries and coastal lagoons that are relatively large, moderately deep, have a moderate watershed size, and are poorly flushed by comparison to estuaries in other regions (Tables 1, 2).

Physical and hydrologic factors such as small tidal range that encourage development of eutrophication were apparent for the majority of the mid-Atlantic estuaries in comparison to, for example, larger tidal range in systems within the North Atlantic. The mid-Atlantic region is among the most densely populated regions within the US (Figure 2).

The Chesapeake Bay estuaries account for 9 of the 22 estuaries within the mid-Atlantic region. This system is a large drowned river valley containing a long, extensive shoreline that includes several major tributary estuaries. The NEEA subdivides the Bay into 9 separate systems for the analysis; the Mainstem, Patuxent, Potomac, Rappahannock, James, Chester, Choptank, and York River estuaries and the Tangier/Pocomoke Sound (Table 2 and nos. 14-22 in Figure 3). The Mainstem consists of a fairly deep (18 m) and narrow (1 – 4 m) channel with higher mean salinities than the tributaries that is derived from ocean waters. The Susquehanna River is the main freshwater source into the upper bay accounting for about 60% of the approximately 2,000 m³ s⁻¹ daily flow. A two-layer density structure is apparent during all seasons of the year with salinity variability more apparent near the head of the bay. Tidal height is typically about 0.9 m near the mouth and decreases

to less than 0.3 m near the head of the bay. Chesapeake Bay has had areas of anoxia and recognized eutrophication problems for many years.

APPROACH

Eutrophication Assessment:

The NEEA evaluates eutrophication using three indices, influencing factors, eutrophic condition, and future outlook and then combines results into one overall rating called ASSETS (Figure 1). Factors influencing eutrophication are nitrogen load (primarily human related sources) and the estuary's susceptibility to develop eutrophication problems which is based on dilution and flushing capabilities. Eutrophic condition is based on assessment of 5 symptoms: chlorophyll a (Chl a, a measure of phytoplankton biomass), macroalgae, dissolved oxygen (DO), submerged aquatic vegetation (SAV) and nuisance/toxic bloom events. Eutrophic condition is determined by evaluating the occurrence of problems as well as the spatial coverage and frequency of occurrence of problem levels of these symptoms. Future outlook for year 2020 is predicted based on expected changes in nutrient loads and the estuary's susceptibility (described above). The influencing factors, overall eutrophic condition, and future outlook results are combined into one rating called ASSETS. Completeness and reliability of the assessment is based on the temporal and spatial availability of data.

Data were collected from researchers around

Table 3: Striped bass expected fish catch (per angler per trip) results at mean and predictive conditions. Expected fish catch increases when dissolved oxygen increases.

System	Expected Fish Catch at Aug. 2002 Mean DO	Expected Fish Catch at 5 mg ⁻¹	Expected Fish Catch at 2 mg ⁻¹	Percent Increase from 2 to 5 mg ⁻¹
Patuxent River	(mean = 5.99 mg l ⁻¹) 7.63	6.27	2.16	65.5
Potomac River	(mean = 4.54 mg l ⁻¹) 4.07	4.55	1.45	68.1

the US using an online survey tool (<http://www.eutro.us>) that automatically calculates the results of the three indices and the overall ASSETS rating.

Human-use indicator of eutrophication impacts:

In addition to the NEEA, another study was conducted to develop a socioeconomic or human use indicator to complement the eutrophication assessment. The traditional approach focuses on how human activities affect water quality but recently there has been great interest in documenting how eutrophication affects human uses of coastal waters. The intent was to develop an indicator that could illustrate the impacts of nutrient-related water quality degradation on various human uses of a system. Using model-derived costs, the impact of the degradation might then be translated into economic costs. The difficulty is that most human uses are not well defined by data that can be used with water quality data to conclusively show the link between losses of a use and water quality. The approach taken in two Chesapeake Bay systems, Patuxent and Potomac River estuaries was to use fisheries catch data and water-column DO data to show predictable relationships.

National Marine Fisheries Recreational Fish Catch data for striped bass were used in conjunction with water quality data to develop a human-use impact indicator. The model links changes in fish catch rate for striped bass to changes in DO, taking into account other influencing factors such as avidity of the angler and water temperature.

RESULTS

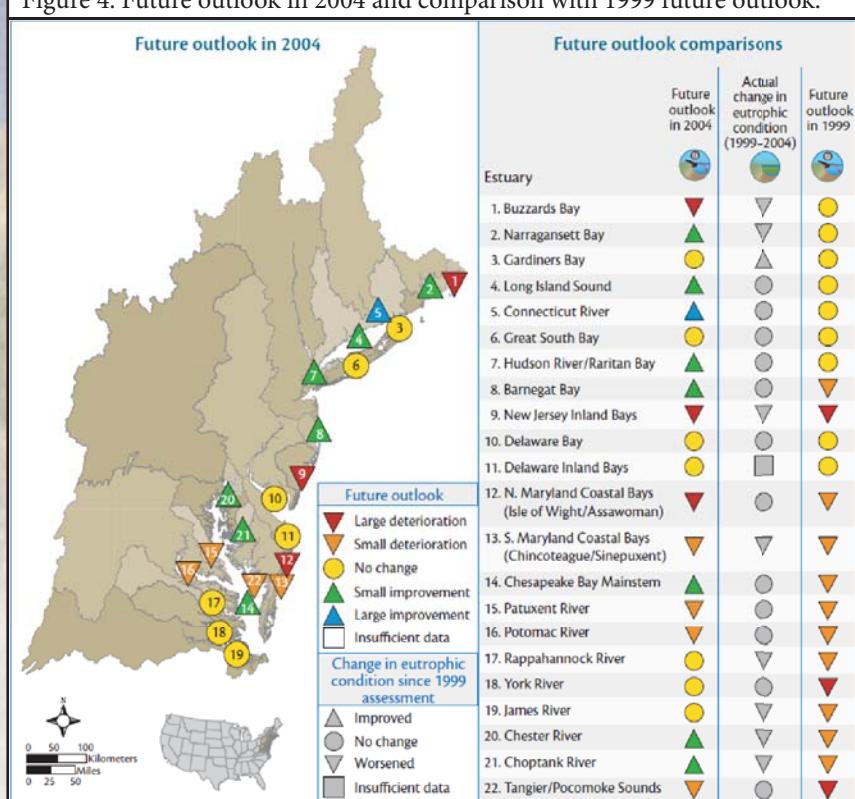
National eutrophication results:

Within the US, the results of the NEEA assessment show that eutrophication is a widespread problem, with the major-

ity of assessed estuaries showing signs of eutrophication—in 65% of the assessed systems, representing 78% of assessed estuarine area, moderate to high overall eutrophic conditions were observed. The majority of estuaries assessed were highly influenced by human-related activities with high influencing factor ratings from New York to Texas, low in the North Atlantic, and mostly unknown in the Pacific region. There were no regional or national patterns of highly eutrophic conditions found, however, the mid-Atlantic region was the most impacted overall (Figure 3). The most common symptoms of eutrophication were high spatial coverage and frequency of elevated Chl a. Survey participants predicted worsening conditions by 2020 in 65% of estuaries and improvements in 20% of estuaries (Figure 4).

An analysis of changes from the early 1990s to the early 2000s showed that conditions in most assessed systems have remained the same (32 systems, 77% as-

Figure 4. Future outlook in 2004 and comparison with 1999 future outlook.



sessed area) with most observed changes reported in smaller systems; 13 systems (9% assessed area) improved and 13 systems (14% assessed area) worsened. However, the assessment of eutrophic condition was impeded by reduced reporting in 2004 as there were inadequate data for 30% of surveyed estuaries, compared to only 12% of estuaries in the early 1990s. This was largely a result of the data collection method; the online survey for the 2004 data versus use of site visits and workshops in addition to a mail survey for the 1999 assessment.

Mid-Atlantic and Chesapeake Bay eutrophication results:

The majority of estuaries within the mid-Atlantic region had moderate to high overall eutrophic conditions; high levels of impacts were observed in 6 of 9 Chesapeake estuaries and moderate high impacts were observed in 3 estuaries (Figure 3). High Chl a conditions were reported for all 9 Chesapeake systems, 7 had moderate to high level problems with nuisance and toxic bloom events, and 5 had moderate to high level problems with DO. Change analysis showed that four of the 9 systems have worse conditions now than in the early 1990s, while conditions in the other 5 have not changed.

Eight of the 9 estuaries are considered to be sensitive or susceptible to development of nutrient related problems on account of natural conditions that make flushing and dilution minimal. This means that even a small input of nutrients can have a large negative impact. Six of the Chesapeake estuaries have high level nutrient loads from human activities within the watershed, with the top 5 causes of resource impacts reported as; wastewater treatment plant effluent, crop agriculture, urban runoff, atmospheric deposition and animal operations. The top impaired uses in Chesapeake estuaries are shellfish, commercial and recreational fishing, fish consumption and aesthetics. Future outlook for these systems is evenly split with 3 systems expected to show improvements in eutrophic condition, 3 expected to remain the same and for 3 systems conditions are expected to worsen in the future (Figure 4).

Human-use indicator results in two Chesapeake Bay estuaries:

The development of an indicator for one of the many possible impacts to human uses of an estuary, in this case fish catch, complements the NEEA method and provides a more complete picture of eutrophication impacts. Results for the Patuxent River estuary, show

that the expected catch at August 2002 mean measured DO concentrations of 5.99 mg/l was 7.63 striped bass per angler per trip. When the DO level is set at 5 mg/l, the corresponding expected striped bass catch drops to 6.27 fish caught per trip (Table 3). When the DO level is set at 2 mg/l the corresponding expected striped bass catch drops to 2.16 striped bass per angler per trip. This represents an increase in fish catch of 65.5% when DO levels change from hypoxic (near 0 mg/l) conditions to dissolved oxygen conditions that are not stressful for fish. For the Potomac River estuary the expected striped bass catch at August 2002 mean measured DO conditions of 4.53 mg/l was 4.07 striped bass per angler per trip. When the DO level is set at 5 mg/l, the corresponding expected striped bass catch increases to 4.55. When the DO level is set at 2 mg/l the corresponding expected striped bass catch drops to 1.45 striped bass per angler per trip. This represents an expected increase in catch of 68.1% when DO levels increase from hypoxic conditions to concentrations that are not stressful to fish (Table 3).

In a different study, results of a model that looks at the conversion to economic terms shows that in the Patuxent River, if DO levels never exceed 5 mg/l, the value of the loss of fish catch to anglers will exceed \$100,000, and is \$300,000 if fishing grounds are anoxic (0 mg/l dissolved oxygen). If all of the Patuxent River had DO levels under 3 mg/l, the net loss to anglers is valued at \$195,000; if the same water quality occurred bay wide, the loss to fishermen is estimated at over \$145 million. Losses are considerably higher as the area impacted by low oxygen conditions increases.

What is being done about eutrophication?

The U.S. Environmental Protection Agency has developed the Chesapeake Bay Total Maximum Daily Load (TMDL), a “pollution diet” that will compel sweeping actions to restore the Chesapeake Bay and its vast network of streams, creeks and rivers. The TMDL was prompted by insufficient progress on bay restoration during the past decade and is required under federal law. The TMDL will be final in December 2010 and is the largest ever developed by EPA. It includes pollution limits that will result in the Bay and its tidal rivers meeting water quality standards and is designed to ensure that all pollution control measures to fully restore the Bay and its tidal rivers are in place by 2025, with 60 percent of the actions completed by 2017.

The Chesapeake Bay TMDL is a keystone commitment in the strategy developed by federal agencies

to meet the President's Chesapeake Bay Executive Order, issued on May 12, 2009. The Executive Order directs the federal government to lead a renewed effort to restore and protect the Chesapeake Bay and its watershed, recognizing that the pollutants that are largely responsible for water quality degradation within the Chesapeake Bay are nutrients. Restoration of the health of the Chesapeake Bay requires a renewed commitment to controlling nutrient pollution from all sources as well as protecting and restoring habitat and living resources, conserving lands, and improving management of natural resources, all of which contribute to improved water quality and ecosystem health. The Federal Government is leading this effort to develop, coordinate and implement programs and activities of agencies participating in protection and restoration of the Chesapeake Bay.

In addition to the federally lead response, universities and state agencies conduct research to learn the magnitude of nutrient related problems within Chesapeake Bay tributaries in an effort to develop strategies in one waterbody that will work in other similar waterbodies. The Corsica River ecosystem study conducted by university and state agency researchers examined the sources of nutrients, the level of impairment of the River and how much the nutrient load would have to be reduced to effect a change in water quality.

Additionally, NOAA is supporting research to explore alternative management measures, specifically the potential for shellfish aquaculture to remove nutrients from coastal waters. Recent research in Chesapeake Bay and elsewhere has shown that shellfish aquaculture has the potential to reduce eutrophication impacts. On-going studies are designed to explore this further and to examine the potential to include aquaculture farmers in TMDL and nutrient trading scenarios. These studies, in addition to the broader scale efforts, will help to develop targeted management measures that will improve water quality and the health of the Chesapeake Bay.

CONCLUSIONS

Eutrophication is a serious problem in National estuaries and in the Chesapeake Bay estuaries with most showing extensive impacts. Impairments include potentially great losses of recreational fish catch. These problems are caused by the natural processing capabilities which make them sensitive to nutrient inputs and to nutrient loads. These loads are from human activities primarily wastewater treatment plants, crop and animal

agriculture activities, urban runoff, and atmospheric deposition. Conditions are expected to become worse in one third of the Chesapeake estuaries by 2020.

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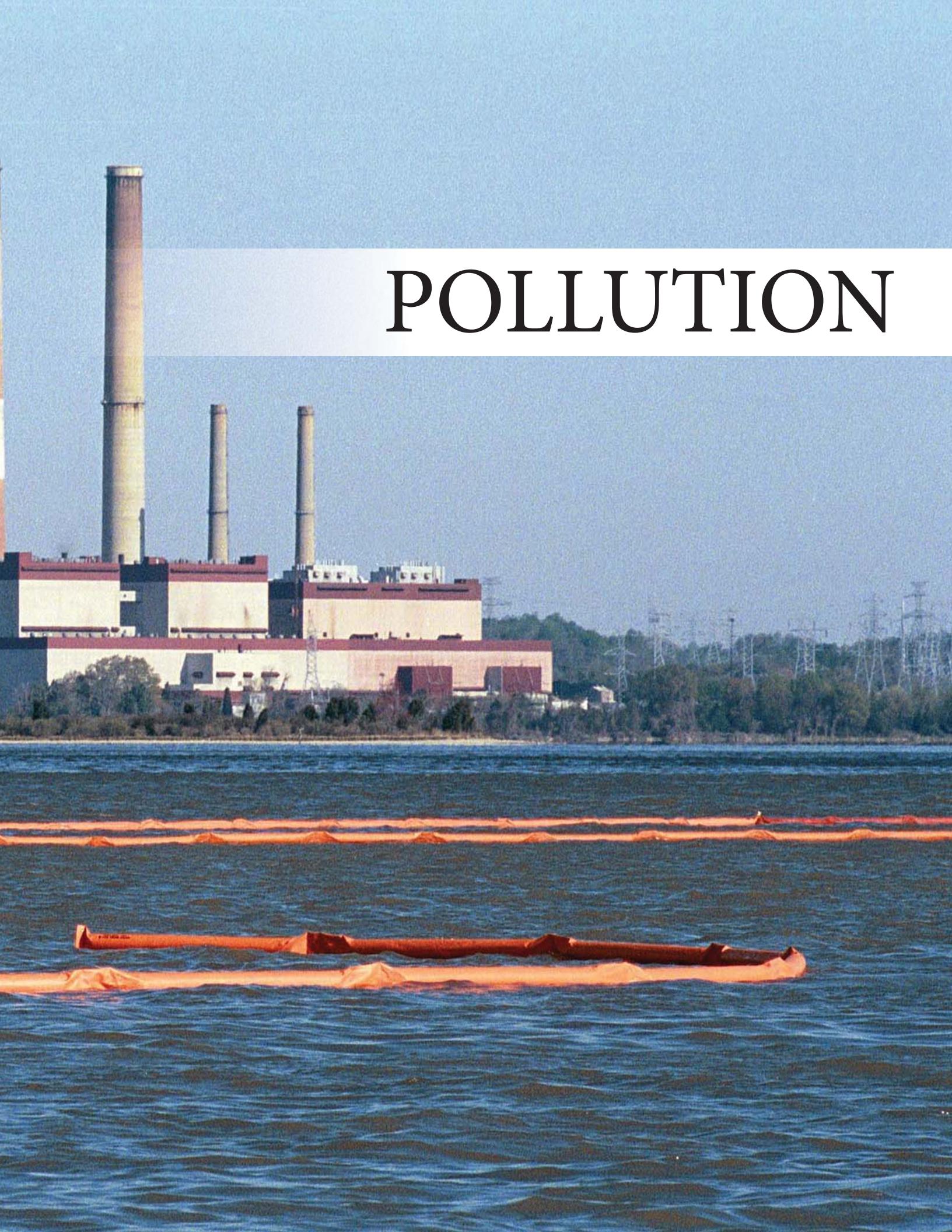
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Farm Aquaculture Resource Management (FARM)
<http://www.farmscale.org>





POLLUTION



CHAPTER 5:

Characterization of Sediment Quality in Five Tidal Rivers of the Chesapeake Bay



M.H. Fulton*, J.L. Hyland, P.B. Key, E.F. Wirth, L. Balthis, C. Cooksey, K. Chung, and A. Leight.

National Centers for Coastal Ocean Science,

Center for Coastal Environmental Health and Biomolecular Research

*Corresponding author, mike.fulton@noaa.gov, 843-762-8576 (phone), 843-762-8700 (fax)

BACKGROUND

Toxic chemical contaminants may enter rivers and estuaries through a variety of pathways that include storm-water runoff, municipal wastewater, non-point source agricultural runoff and industrial point source discharges. Some of these chemicals, such as agricultural pesticides, may be highly toxic but short-lived in the environment. Other toxic contaminants such as polycyclic aromatic hydrocarbons, polychlorinated biphenyls, and metals are more persistent and may accumulate in sediments and biota and cause both acute and chronic toxicity in aquatic organisms. Efforts to assess the effects of toxic contaminants should include an evaluation of these exposure scenarios.

In 1999, the Chesapeake Bay Program (CBP) completed a comprehensive survey of existing data on chemical contaminants and their potential bioeffects in 38 tidal river areas of Chesapeake Bay (CBP 1999). This review led to the identification of 20 areas for which there were either inconclusive or insufficient data to adequately characterize the potential for contaminant bioeffects on the Bay's living resources. In efforts to support goals of the Chesapeake 2000 Agreement (an important partnership set up to protect and restore the Chesapeake Bay ecosystem), the Toxics Subcommittee of the Chesapeake Bay Program subsequently developed a "Toxics 2000 Strategy" with a commitment to: "...update the 1999 Toxics Characterization by conducting the necessary biological and chemical monitor-

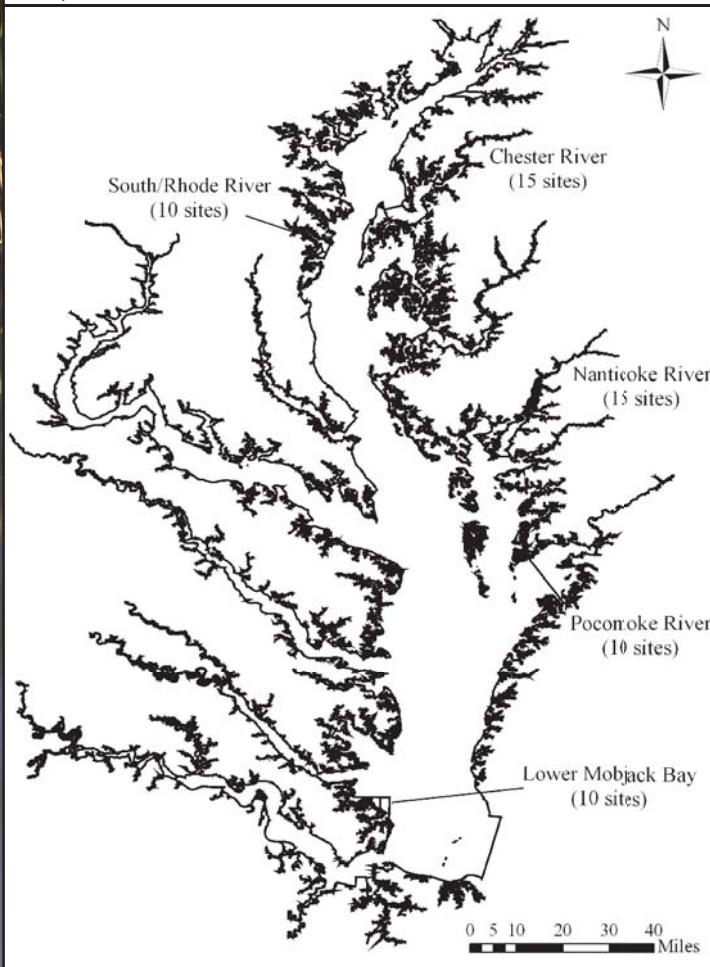
ing to characterize the status of chemical contaminant effects on living resources in those tidal rivers characterized as 'areas with insufficient or inconclusive data' and in the mainstem Bay."

Data from a variety of more recent federal, state, and CBP studies that were not available at the time of the 1999 Toxics Characterization helped to fulfill this commitment. Such studies were identified in a subsequent analysis of data gaps conducted by the Toxics Subcommittee and included in their Three-Year Budget Plan (March 2001). However, additional data were still needed for those waters where new data were not being collected or where recent findings were inconclusive and needed to be substantiated.

APPROACH

The main objective of the present study was to estimate the current status in ecological condition of five such river areas of the Chesapeake Bay and thus to help complete the overall toxics inventory goal for the bay. These systems included the Chester River, Nanticoke River, Pocomoke River, Lower Mobjack Bay (Poquoson and Back Rivers), and the South and Rhode Rivers (Figure 1). The study utilized a Sediment Quality Triad (SQT) approach. The SQT approach provides a means to assess the condition of these estuaries from the perspective of sediment quality, based primarily on combined measures of sediment contamination, sediment toxicity, and condition of ambient benthic fauna.

Figure 1. Five river areas of the Chesapeake Bay included in the study.



Combining such measures in this fashion has been shown to be very effective as a “weight-of-evidence” approach to assessing pollution-induced degradation of the benthos, especially in relation to persistent sediment-associated contaminants (Long and Chapman 1985, Chapman 1990).

A total of 60 stations were distributed among the five systems, using a probabilistic random design (Figure 1). This design allowed for unbiased statistical estimates of the spatial extent of degraded versus non-degraded condition. At each station, there was synoptic sampling of a variety of ecological indicators — including general habitat characteristics, multiple stressor levels, toxicity, and biological responses — to support “weight-of-evidence” assessments of condition and to allow for the examination of potential associations between the presence of stressors and potential bioeffects. Sediment samples for chemical contaminant analysis, total organic carbon (TOC), acid volatile sulfide (AVS), grain-size analysis, toxicity testing (juvenile clam; amphipod), and benthic community assessments were collected at each station. Samples were collected and ana-

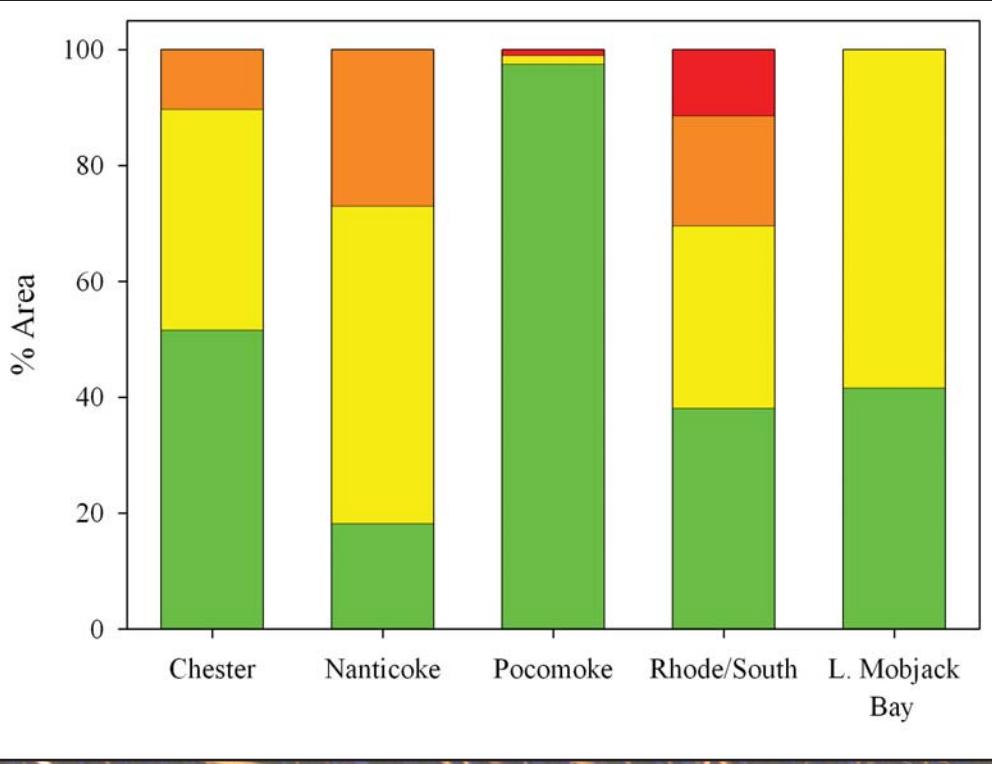
lyzed using established protocols (See Fulton *et al.* 2007 for detailed methodology).

The overall characterization of sediment quality for the five river systems was based on combined measures of benthic condition (B-IBI, Weisberg *et al.* 1997, Llanso *et al.* 2002), sediment toxicity (significant toxicity in both the 10-day juvenile clam and *Leptochirus* amphipod assays), and sediment contamination (≥ 1 ERM exceedance or mean ERMQ >0.098). Stations were assigned to one of four categories based on these three legs of the SQT. Figure 2 provides a geographical comparison of the percent area represented by stations within each of the categories. Green stations (high sediment quality) were those with no hits for any of the three legs of the triad; stations with one hit coded yellow (moderate sediment quality); orange stations (marginal sediment quality) had hits on two legs of the triad; and red stations (poor sediment quality) had hits for all three legs.

KEY FINDINGS

- In the Chester River, 51.6% of the total area coded green, 38.0% coded yellow, 10.3% coded orange, and none of the area was coded red. Stations coding yellow in this system generally had sediments that produced toxicity, but did not have degraded benthos or evidence of elevated levels of sediment contamination. Stations coding orange generally had toxic sediments and a degraded benthos, but no elevation of sediment contamination. One possible explanation for the toxicity and/or degraded benthos without evidence of elevated contaminant levels in sediments could be the presence of unmeasured contaminants transported to the system in nonpoint source runoff (McConnell 2005). An additional explanation for the increased toxicity in the bioassays may have been related to physicochemical characteristics of the sediments. Most of the stations that produced toxicity in the bioassays were from the upper and middle sections of the river and were characterized by stations with low pH and salinity. Overall, in the Chester River, evidence of high sediment quality, with healthy benthic assemblages and no significant toxicity or chemical contamination, was observed in over half (52%) of the area, while matching evidence of degraded condition based on co-occurring hits in two or more legs of the SQT was found in a small portion (10%) of the river.

Figure 2. Geographical comparison of the percent area represented by stations within each of the categories.



- In the Nanticoke River, only 18.2% of the area coded green, 54.7% coded yellow, 27.0% coded orange, and none of the area coded red. Yellow stations were those that had either degraded benthos or toxic sediments with no linkage to high levels of measured contaminants. Adverse exposure conditions associated with high TOC may have contributed to degraded benthic condition at several of these sites.
- The Pocomoke River had 97.5% of the area coded green, 1.5% coded yellow, and 1% coded red. Thus, high sediment quality was more spatially extensive in this system than in any of the other rivers surveyed.
- The Rhode/South system had the highest levels of sediment-associated contaminants of any of the five river systems sampled. It also had the highest percent area coding red (11.4%), revealing strong evidence of contaminant-induced degradation of the benthos. The stations coding orange in this system were generally those with hits for benthic degradation and exceedances of contaminant bioeffect thresholds. There was a much lower incidence of toxicity. The high levels of both TOC and AVS in the sediments at many of the sites in the Rhode/South system may have reduced the bioavailability of organic and inorganic contaminants and thus reduced the toxicity of the sediments in the bioassays. The organic enrichment of sediments, as evidenced by high TOC in excess of associated bioeffects thresholds, may have contributed to degraded benthic condition at several of the sites.

degraded benthos in the absence of exceedances of contaminant thresholds or bioassay toxicity. Possible explanations for the degraded benthos include: (1) impacts were due to unmeasured chronic stressors and the short-term bioassays were less sensitive to such stressors; (2) benthic impacts were caused by other natural disturbances (e.g. storm scour, erosional effects; or (3) some variability and uncertainty in the predictive ability or classification efficiency of the B-IBI.

CONCLUSIONS

A comparison of the systems sampled in this study indicates that only two of the systems had any stations coding red with hits on all three legs of the SQT. In the Rhode/South system this represented 11.4% of the total area while in the Pocomoke such highly degraded stations represented only 1% of the total area. All of the river systems had > 65% of the area with sediment quality coding as either high (green) or moderately good (yellow). The Chester, Nanticoke, and Lower Mobjack Bay systems had the least evidence of sediment-associated contaminants with only one station in the first two systems and no stations in Lower Mobjack Bay having contaminant levels that exceeded the defined contaminant bioeffect thresholds. In the Chester River particularly, however, there was evidence of non-

ity of organic and inorganic contaminants and thus reduced the toxicity of the sediments in the bioassays. The organic enrichment of sediments, as evidenced by high TOC in excess of associated bioeffects thresholds, may have contributed to degraded benthic condition at several of the sites.

- The Lower Mobjack Bay system was the least contaminated of the five systems studied based on the levels of contaminants measured in sediments. In this system, 41.6% of the area coded green and 58.4% coded yellow. All of the hits in this system were associated with

point source inputs of pesticides. Many of the stations in Rhode/South system had relatively high levels of sediment-associated organic and inorganic contamination. Although ERM exceedances were rare, many of the stations had a large number of ERL exceedances. Of the systems sampled, the Pocomoke River had by far the largest proportion of estuarine area with high sediment quality.

The results of this study highlight the importance of using multiple indicators and a weight of evidence approach to characterize environmental/sediment quality and the potential bioeffects of toxic contaminants. The potential for sediment-associated contaminants to cause toxicity is greatly affected by physicochemical factors that can alter bioavailability; thus an assessment should not be based on contaminant levels alone. Laboratory sediment bioassays are sensitive to a variety of factors including the physicochemical characteristics of the sediments. Additionally, bioassays are generally of relatively short duration and may be less sensitive to long-term chronic effects reflected in the benthos. Benthic indicators can be affected by a variety of unmeasured stressors and non-contaminant environmental factors. Thus, the assessment approach used in this study assigned equal weights to each of three indicators and scored each station and river system based on a weight of evidence approach.

ACKNOWLEDGMENTS

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CHAPTER 6:

Sediment Quality Assessment: Chesapeake Bay Bioeffects Studies



S. Ian Hartwell*

National Centers for Coastal Ocean Science,
Center for Coastal Monitoring and Assessment

*Corresponding author, ian.hartwell@noaa.gov, 301-713-3028 x137 (phone), 301-713-4384 (fax)

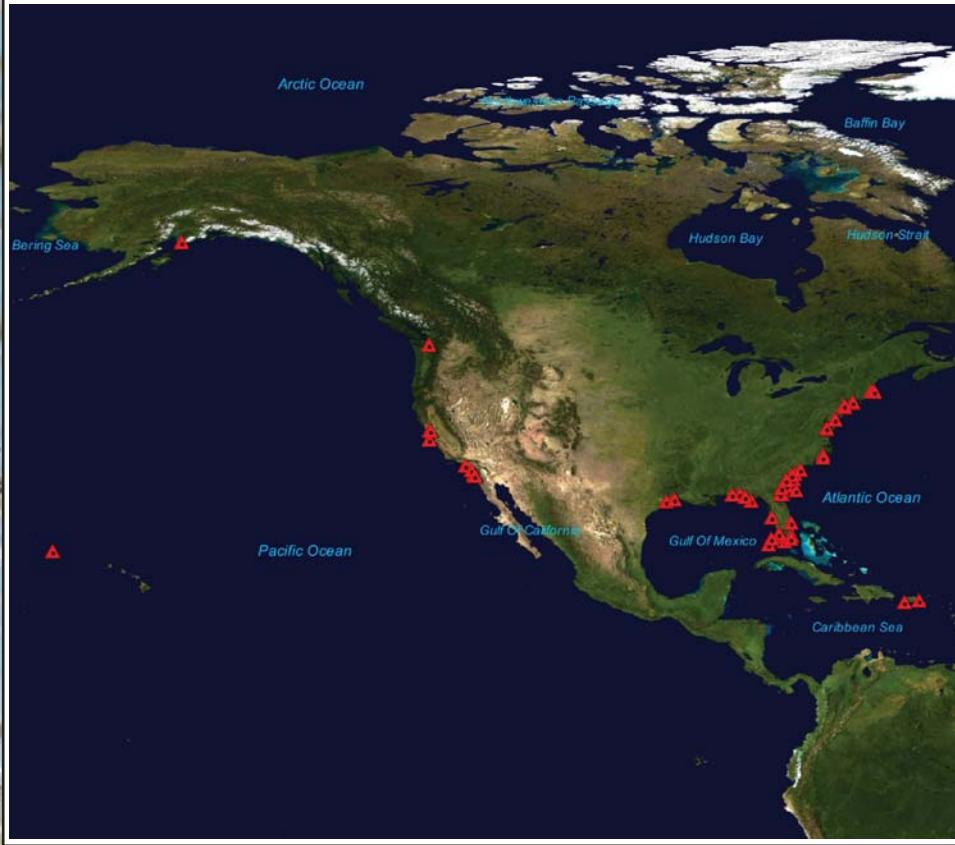
INTRODUCTION

Through the National Status and Trends (NS&T) Bioeffects Program, NOAA has conducted studies to determine the spatial extent and severity of chemical contamination and associated adverse biological effects in coastal bays and estuaries of the United States. The Bioeffects program is a nationwide program of environmental assessment and related research designed to describe the current status of environmental quality in our Nation's estuarine and coastal areas. Field studies examine the distribution and concentration of chemical contaminants in sediments, measure sediment toxicity, and assess the condition of bottom-dwelling biological communities. This information is integrated into a comprehensive assessment of the health of the marine habitat. Bioeffects projects assess the spatial distribution and magnitude of effect of chemical contamination, and develop indicators of environmental contaminant exposure in water bodies, ranging from small estuaries to large bays and coastal areas. Over 30 multidisciplinary studies have been carried out since 1991 in close cooperation or in partnership with coastal states or regional organizations. Data generated by the Bioeffects Program are used to assess the distribution, concentration and magnitude of chemical impacts at a given location, and over broad spatial scales. Data are applicable to environmental risk assessments, damage assessments, and for planning future resource management and restora-

tion activities. Utilization of consistent methods over the life of the program allows for comparison of the magnitude and extent of contaminant effects relative to other locations throughout the US, and over time. All data are generated following strict performance-based quality control and quality assurance protocols. Data are available to regional, federal, state and local resource managers and the public via publications, presentations and a website data portal.

Bioeffects surveys are conducted in specific coastal regions where contaminant monitoring data from NOAA's National Status and Trends Program – and information from state and local sources – indicate that the potential for substantial environmental degradation and associated biological effects exists. Bioeffects assessment studies consist of: 1) sediment toxicity, 2) sediment contamination, and 3) sediment biological community surveys; otherwise known as the Sediment Quality Triad approach (SQT) (Chapman *et al.* 1987). SQT assessments are considered in the context of natural background habitat conditions and stressors. Sediment toxicity assessments are based on a suite of bioassays that assess different levels of effect and exposure. These may include direct effects of acute mortality and/or sub-lethal effects of impaired fertilization, abnormal larval development, physiological stress, and biomarkers of exposure to specific chemical contaminants. Tests may be conducted with whole sediment, water trapped

Bioeffects study sites in the US.



between sediment particles (pore water), or organic extracts from sediments. Chemical contamination assessments include the entire NS&T suite of organic and trace element contaminants. Biological assessments describe the biological community condition and species patterns from a site specific to system-wide scale.

Critical habitats and food chains supporting many estuarine fish and wildlife species involve the benthic environment. Contaminants in the sediments often pose both ecological and human-health risks through degraded habitats, loss of fauna, biomagnification of contaminants in the coastal ecosystem, and human consumption of contaminated fish and wildlife. In many instances, fish consumption advisories are coincident with severely degraded sediments in coastal water bodies. Thus, characterizing sediment quality by describing benthic assemblage and delineating areas of

sediment contamination and toxicity are viewed as important goals of coastal resource management. Benthic community studies have a history of use in regional estuarine monitoring programs and have been proven to serve as an effective indicator for describing the extent and magnitude of pollution impacts in estuarine ecosystems, as well as for assessing the effectiveness of management actions.

Chesapeake Bay is the largest estuarine system in the continental United States. Including tidal tributaries, the Bay has approximately 18,694 km of shoreline (more than the entire US West Coast). The watershed is over 165,000 km² (64,000 miles²), and includes portions of six states (Delaware, Maryland, New York, Pennsylvania, Virginia, and West Virginia) and the District of Columbia. The population of the

watershed exceeds 15 million people. There are 150 rivers and streams in the Chesapeake drainage basin. Within the watershed, five major rivers—the Susquehanna, Potomac, Rappahannock, York and James—provide almost 90% of the freshwater to the Bay. The Bay receives an equal volume of salt water from the Atlantic Ocean.

Toxic contaminants enter the Bay via atmospheric deposition, dissolved and particulate runoff from the watershed or direct discharge. While contaminants enter the Bay from several sources, sediments accumulate many toxic contaminants and thus reveal the status of input for these constituents. In the watershed, loading estimates indicate that the major sources of contaminants are point sources, stormwater runoff, atmospheric deposition, and spills. Point sources and urban runoff in the Bay proper contribute large quantities of contaminants. Pesticide inputs to the Bay have



not been quantified. Baltimore Harbor and the Elizabeth River remain among the most contaminated areas in the United States.

In the upper Bay and tributaries, sediments are fine grained silts and clays. Sediments in the middle Bay are mostly made of silts and clays derived from shoreline erosion. In the lower Bay, by contrast, the sediments are sandy. These particles come from shore erosion and inputs from the Atlantic Ocean. The introduction of European-style agriculture and large scale clearing of the watershed produced massive shifts in sediment dynamics of the Bay watershed. As early as the mid 1700s, some navigable rivers were filled in by sediment and sedimentation caused several colonial seaports to become landlocked.

In the mainstem, deep sediment core analyses indicate that sediment accumulation rates are 2-10 times higher in the northern Bay than in the middle and lower Bay, and that sedimentation rates are 2-10 times higher than before European settlement throughout the Bay (NOAA 1998). The core samples show a decline in selected PAH compounds over the past several decades, but absolute concentrations are still 1 to 2 orders of magnitude above pristine conditions. Core data also indicate that concentrations of PAHs, PCBs and, organochlorine pesticides do not demonstrate consistent trends over 25 years, but remain 10 times lower than

sediments in the tributaries. In contrast, tri-butyl-tin (TBT) concentrations in the deep cores have declined significantly since its use was severely restricted.

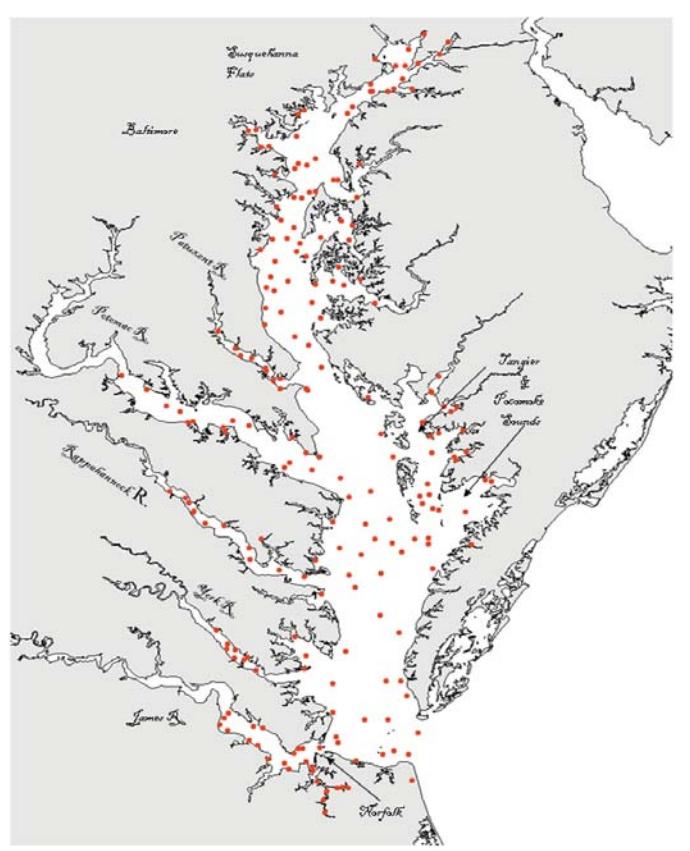
METHODS

The NS&T Program uses a stratified-random sampling design to determine the spatial extent of sediment contamination and toxicity. Chesapeake Bay was divided into sixty-five strata based on the knowledge and recommendations of scientific researchers and resource management agencies. A minimum of three sampling sites within each stratum were selected on a random basis. The focus of the sampling design was the larger open expanses of the Bay system. A total of 210 sites were sampled.

Sediment samples were taken at each site in accordance with standard methods developed by the NS&T Program. Samples were taken for toxicity bioassays, chemical contaminant analysis, and benthic community assessment. Only the upper 2-3 cm of the sediment was taken in order to assure collection of recently deposited materials.

Amphipod mortality, sea urchin fertilization impairment, Microtox[®] luminescence, and cytochrome P450 Human Reporter Gene System (HRGS) tests were carried out by contract laboratories on sediment samples or extracts. A broad suite of chemicals were analyzed at each station, including 13 metals, butyl-tins, PAHs, chlorinated compounds (PCBs, chlorinated pesticides, furans and dioxins). In addition several physicochemical measures of sediment properties (e.g. grain size, TOC, etc.) were determined. Quantitative benthic community characterizations included enumeration of species composition and calculation of density, species richness, evenness, and diversity indices.

Correlation coefficients were calculated between all chemical, toxicological and biological metrics. Regressions were calculated to assess relationships between toxicological, community, contaminant, and habitat attributes. Regressions of toxicity, community, contaminant and habitat indices against % silt clay content were calculated and the residuals were used to assess regression relationships between them in the absence of the influence of grain size. Multivariate cluster analysis was used to group site and species data. A nodal analysis routine was then applied to those results combining the cluster analyses in a graphical array. The objective of the nodal analysis was to produce a coherent pattern of association between results for sites and species clusters. Principal component analysis (PCA)



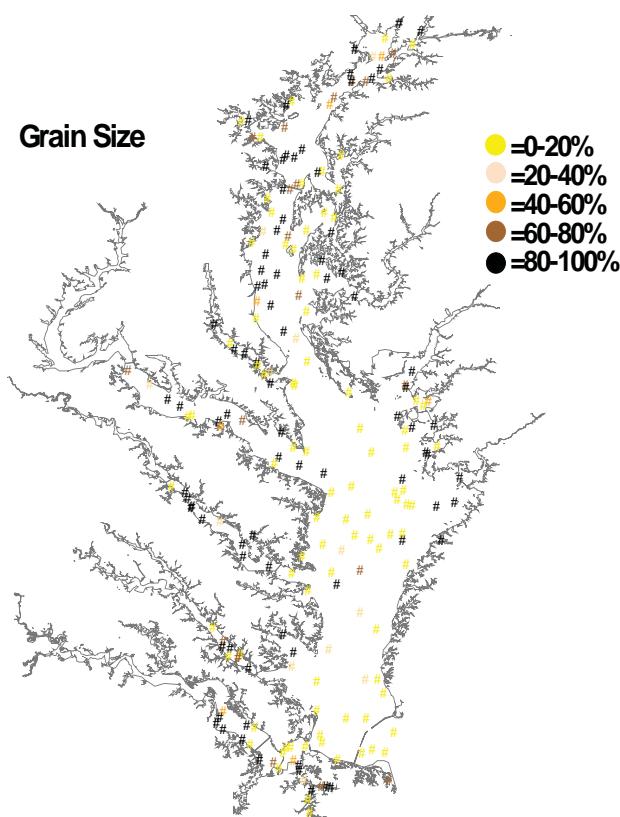
was used to group the sampling sites using benthic community, contaminant, and toxicity metrics. Calculation of a Sediment Quality Triad (SQT) index was developed to quantify impact, and results were compared to the distribution of known stressors (contamination, hypoxia).

RESULTS

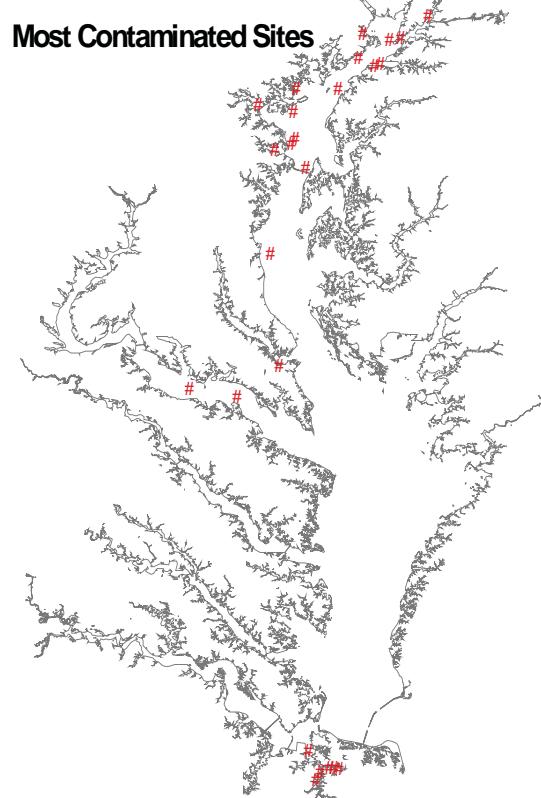
Sediments in the tributaries tended to be mudier upstream and coarser near the mouths of the rivers, however sandbars were present in all locations. Sediments in eastern shore embayments also tended to have finer grained sediments than the mainstem. Sediments in the deep trough were uniformly fine grained depositional material. Most of the sampled locations in the Susquehanna Flats contained fine grained material.

Most of the mainstem of the Bay was relatively uncontaminated. Depositional areas in the Susquehanna Flats area and the upper portions of the deep trough had higher concentrations of contaminants than the middle and lower Bay. Most tributaries had higher contaminant concentrations than the mainstem. Of the large western tributaries, the Potomac and the James Rivers showed the most elevated concentrations. Most embayments were as clean as the lower mainstem, with the exception of areas off the Gunpowder River above

Percent fine grained sediment.



Distribution of sites in the top 10th percentile of contamination concentration.



Baltimore, and nearshore stations in Tangier and Pocomoke Sounds, where pesticide concentrations were elevated. Virtually all of the sites comprising the top 10th percentile of contaminated sites were found in the Elizabeth River, Baltimore Harbor, and the Susquehanna Flats or the deep trough. In the tributaries, the load of PAHs have a larger proportion of pyrogenic (e.g. combustion by-products) compounds than in the mainstem. The distribution of metals was similar to the organic contaminants. Metals concentrations were elevated at the one station in the vicinity of Hart Miller Island. Chlorinated pesticides were found throughout the Bay. The distribution of elevated concentrations was compound specific. Concentrations of TBT in the Susquehanna flats, while elevated compared to the lower mainstem sites, were not typically as high as several of the tributary stations.

Most significant toxicity responses were from stations in the Susquehanna Flats and the tributaries, however this was test-specific. None of the amphipod bioassays yielded significant toxicity. In contrast, 73 of the sea urchin fertilization bioassays were significant. The HRGS P450 bioassay showed responses at most of the stations in the Susquehanna Flats, the deep trough, the Potomac and Elizabeth Rivers, and some other scattered sites. The spatial extent of impaired habitat (as

defined by significant observed toxicity) varied widely. Based on strata areas, the spatial extent of impaired habitat ranged from zero to 30.6% depending on the selected bioassay.

A total of 20,609 organisms, representing 287 taxa were enumerated. Polychaete and oligochaete worms were the most dominant group, both in terms of organism abundance and number of taxa. Clams and snails were the next most abundant taxa, but were characterized by very high numbers of a relatively few species. The vast majority of crustaceans were amphipods. Species richness was site specific, varying considerably from one site to the next. Abundance varied by several orders of magnitude, even in adjacent sampling stations.

A pattern of species distribution appears when the data are condensed on a stratum by stratum basis. The constricted region of the Bay west of Kent Island and south of the Bay Bridge had a generally low species richness. This area is dominated by deep trough habitats and the associated anoxic/hypoxic oxygen stress. There were fewer species in the western tributaries corresponding to the deep areas in the Patuxent, Potomac, and Rappahannock Rivers. The lowest values in the mainstem were from the central deep trough. The highest values were near the mouth of the Bay. Abundance by strata generally followed the same outline as species

richness, but with greater variability between strata.

The community attributes of species richness, abundance, and diversity were significantly, and negatively correlated with all but one of the contaminant groups. They were also consistently negatively correlated with the bioassay results. All significant regression slopes were negative. Observed toxicity and contaminant parameters showed positive, and highly significant regression relationships. The percent silt/clay, TOC and chemical concentrations all demonstrated relatively high correlation. Using the residuals from regression of the community, toxicity, and contaminant parameters on percent silt/clay, none of the community attributes demonstrated significant regressions with the chemical contaminant indices. In contrast, species number, abundance and diversity still showed significant negative regression relationship with toxicity.

Cluster analyses resolved into nodes for 1-Susquehanna Flats, 2- the upper Bay between Baltimore and the Choptank River plus the upper reaches of the major western tributaries, 3- Tangier Sound and the lower reaches of the western tributaries, 4- sandy sites throughout the lower Bay, 5- the Bay mouth. These latter three had overlapping, but distinct community makeup. In contrast, the Susquehanna Flats node and upper Bay/upper tributary node shared fewer species, and these tended to be cosmopolitan taxa.

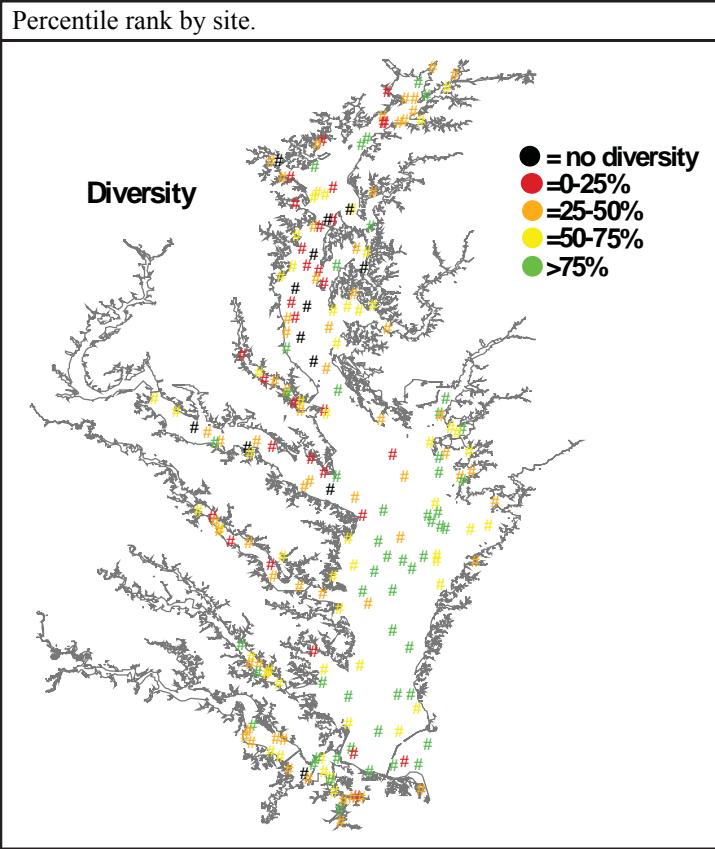
The PCA procedure produced discernible patterns. The most contaminated sites in the Elizabeth River and Baltimore Harbor were separated from all other sites. The SQT calculations indicated a relationship between chemical contamination and species diversity. Furthermore, sites that are stressed primarily by chemical contamination can be distinguished from sites with other impacts (e.g. hypoxia), but the latter sites are generally subject to multiple stressors.

DISCUSSION

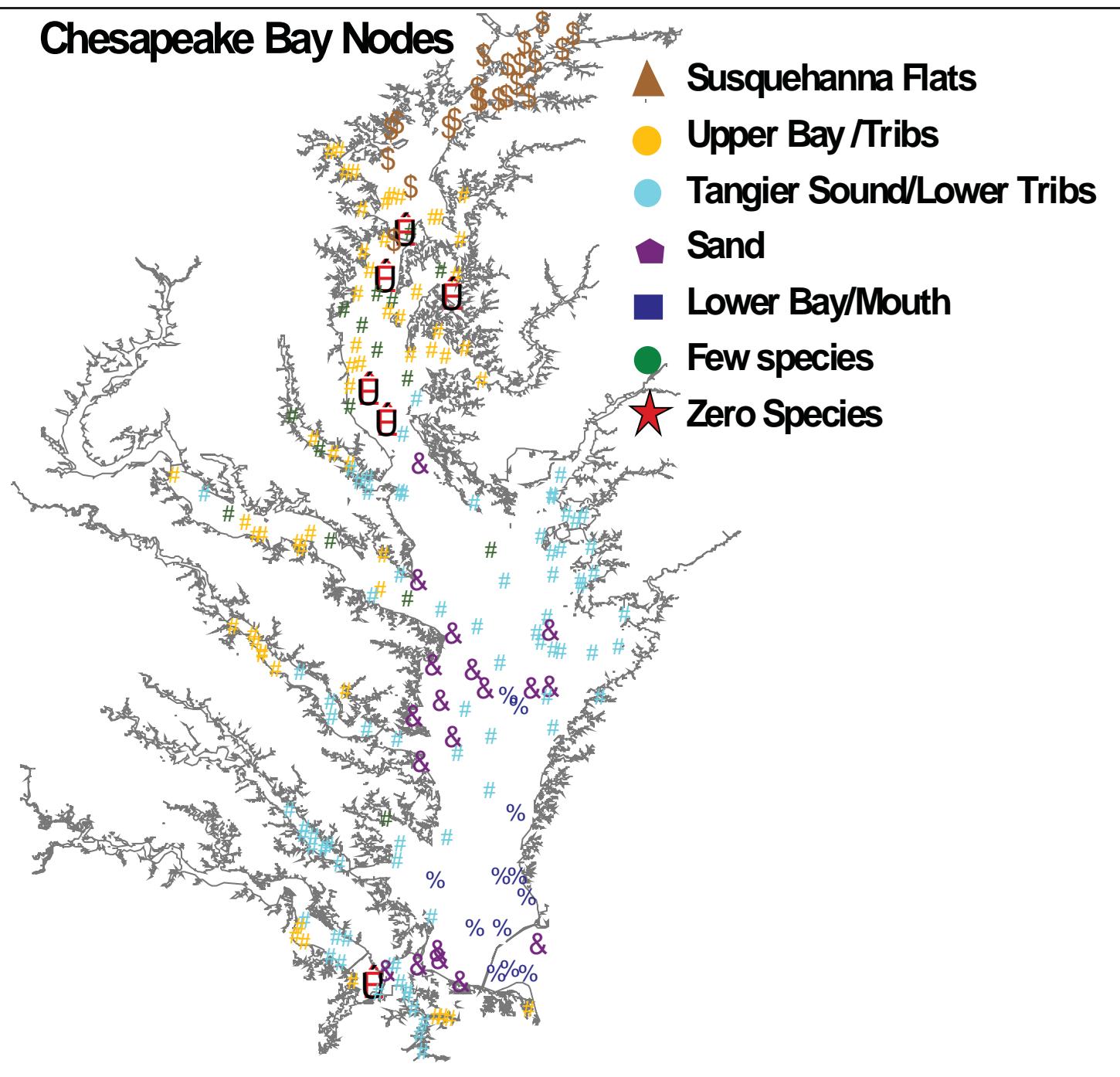
Salinity and grain size were the primary factors which determine community distributions in the Chesapeake Bay mainstem. Each of the major western tributaries also contained distinct mesohaline and polyhaline communities that mimicked the distribution in the mainstem, although they were not physically connected and maintain themselves independently in each subsystem.

Chemical contamination and toxicity responses are more closely correlated to each other than either of these two parameters are with benthic community metrics. When viewed in detail, the benthic community

Percentile rank by site.



Distribution of species association nodes in Chesapeake Bay.



does respond to contamination in measurable fashion, however, certain relationships need to be understood to clarify the relationships.

Diversity, and number of species declined with increasing chemical concentrations. This was partly due to the distribution of fine grained sediments, where elevated contaminant levels were found, and the characteristics of the resident communities in fine grained vs sandy sediments. The nodal analysis demonstrated that the resident communities found in those areas are inherently different from the areas with coarser grained sediments. However, observed toxicity increased with

increasing contaminant values, and that impact cannot be ignored when evaluating community impact patterns. When viewed in terms of a habitat-specific community assemblage, as derived from the nodal analysis, biological indices indicated detectable impact of contaminants. Abundance did not decline as sharply as species numbers with increasing contamination, suggesting that pollution tolerant species are able to grow and reproduce in contaminated areas in the absence of competitors, predators, and/or indirect effects on the habitat. In the most stressed areas, all biological indices declined.

Normalizing community indices for grain size yielded a relationship between them and contaminant level. The lowest normalized diversity values were from the sites dominated by pollution tolerant species. Thus, low values of grain size normalized diversity was a consistent indicator of stressed conditions in all areas, but distinguishing contaminant stress responses from other stressors (e.g. hypoxia) may not be possible with this approach. The SQT approach does distinguish between contaminant vs other stressors, but it cannot distinguish the relative contribution of different types of stressors.

Grain size distribution also explained the variation in the distribution of contaminated and uncontaminated areas in Baltimore Harbor and the Elizabeth River. Within those systems, sandy sites did not contain contaminants at levels as high as those found at the muddy sites. TOC normalized PAH data illustrates that all Elizabeth River and the Baltimore Harbor sites had elevated PAH concentrations relative to most other areas. Normalized concentrations in the deep trough were relatively low away from the mouths of tributaries, but concentrations in the Susquehanna Flats were not. Normalization for grain size yielded a similar picture for metals. Thus loading rates (and/or residual deposits) in the Elizabeth River and in the vicinity of Baltimore Harbor and the Susquehanna River are elevated.

Previous studies in Baltimore Harbor demonstrate steep gradients in contaminant concentrations from the heads of the various tributaries down into the Patapsco subestuary (Baker et. al. 1997). Concentrations reported in this NS&T study were considerably lower than what has been reported at locations upstream in the Patapsco system. In previous studies of the Elizabeth River, contaminant concentrations were also seen to be highly variable on a site specific basis due to a combination of historical sources of pollution and sediment characteristics. The Eastern Branch contaminant concentrations were as high, if not higher, than the Southern Branch even though the Eastern Branch is primarily residential along the shoreline of the upper reaches.

The Hart Miller Island containment facility is the repository for dredge spoil from Baltimore Harbor and approach channels. The single NS&T station in the Hart Miller Island area showed elevated metals levels relative to the surrounding area. Even after grain size normalization, the station demonstrated higher concentrations of metals relative to other stations.

The distribution of high and low weight PAHs, and the degree of alkylation indicated a pyrogenic

source for the high molecular weight PAHs. The low molecular weight PAHs are likely a mixture of pyrogenic sources and fuel spills. The median concentration of PAHs in the tributaries was five times that found in the mainstem or embayments.

The mass of various contaminants in the upper 10 cm of sediment for different depositional compartments of the Chesapeake Bay mainstem were calculated (Table A). The northern portion of the Bay, including Susquehanna Flats, the Patapsco, and Chester Rivers contain a much higher reservoir of contaminants than other areas. On an areal basis however, the concentrations found in the deep trough were comparable. In contrast, Tangier Sound contained vastly less contamination than Susquehanna Flats. The Elizabeth River, although relatively small in size contained significant quantities of contaminants. The concentrations of PAHs were an order of magnitude higher in the Elizabeth River than any other region. Average metal concentrations were found in the Elizabeth River at concentrations comparable to those in the northern region of the Bay. The areas in Hampton Roads and Norfolk cannot be compared in the same way because the sediments are sandy. While industrial, and shipping-related activity is intense, sediment in Hampton Roads were not as contaminated as one might presume because it is not a depositional environment, and it is well flushed.

Relative to background values, the Chesapeake is enriched for most elements even in the relatively clean area of Tangier sound. This is due to the depositional nature of an estuary. Enrichment in the Susquehanna Flats exceeded Tangier Sound for every element except Cr. Enrichment levels in Elizabeth River were low for As, Cr, and Ni, but higher for all the others. Enrichment of Se and Hg were especially high. The single muddy site in Baltimore Harbor (# 23) showed the highest enrichment rates of any location in the Bay. The Elizabeth River was also contaminated with metals, but not to the same concentrations as the Patapsco.

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Region	Northern Bay		Deep Trough		Tangier Sound		Elizabeth River	
Strata	1-9		11,14,19		33-40		62-64	
Area (km ²)	1135.0		333.5		1174.1		14.9	
	kg	kg/km ²	kg	kg/km ²	kg	kg/km ²	kg	kg/km ²
PAH	219,415	193	44,845	134	50,017	43	16,420	1,100
PCB	1,667	1	326	1	716	1	89	6
DDT	454	0.4	35	0.1	145	0.1	42	3
Chlordanes	113	0.1	14	0.04	77	0.07	12	1
As	1,738,872	1,532	642,942	1,928	758,368	646	21,283	1,426
Cd	82,798	73	25,243	76	23,106	20	1,047	70
Cr	12,006,975	10,579	3,850,546	11,545	5,341,199	4,549	115,201	7,717
Cu	5,579,045	4,915	1,580,890	4,740	1,456,042	1,240	126,507	8,474
Pb	6,599,546	5,814	1,887,153	5,658	2,300,265	1,959	102,645	6,876
Hg	23,165	20	5,063	15	3,661	3	560	38
Ag	58,803	52	13,067	39	6,295	5	620	42
Ni	7,555,691	6,657	1,910,015	5,727	2,232,902	1,902	46,254	3,098
Se	128,775	113	48,571	146	56,465	48	2,605	174
Zn	32,824,582	28,920	9,613,109	28,824	9,056,296	7,713	502,461	33,657

CHAPTER 7:

Assessment of Water Quality in the Choptank River Estuary



David Whitall^{1*}, and Andrew K. Leight²

National Centers for Coastal Ocean Science,
Center for Coastal Monitoring and Assessment¹,
and Center for Coastal Environmental Health and Biomolecular Research, Cooperative Oxford Laboratory²

*Corresponding author, dave.whitall@noaa.gov, 301-713-3028x138 (phone), 301-713-4384 (fax)

POLLUTION

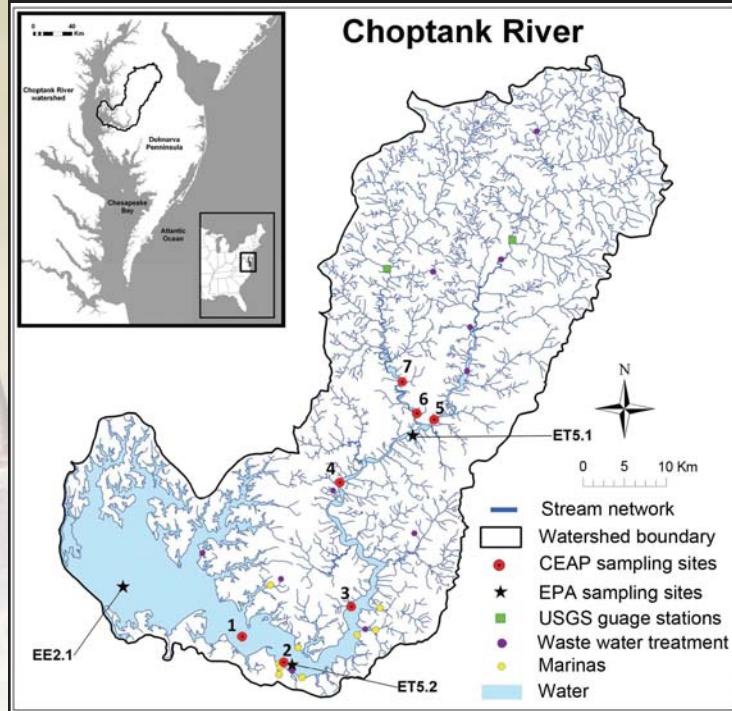
BACKGROUND

One of the more well-studied tributaries within the Chesapeake Bay watershed is the Choptank River. The University of Maryland Horn Point Laboratory and the National Oceanic and Atmospheric Administration (NOAA) - Oxford Marine Laboratory are both located within its watershed, facilitating a number of long term ecological studies and water quality data collection (Fisher *et al.*, 2006a, 2006b; Sutton *et al.*, 2009; Pait and Nelson, 2009). Additional studies of the Choptank River have been carried out by Maryland Department of Natural Resources, United States Department of Agriculture - Agricultural Research Service (USDA-ARS), and United States Geological Survey (USGS) (Ator *et al.*, 2004; Goel *et al.*, 2005; Kuang *et al.*, 2003; Lehotay *et al.*, 1998). The Chesapeake Bay Water Quality Monitoring Network includes three stations in the Choptank River estuary (Figure 1), and this watershed has also been included in a national study of agricultural best management practices called the Conservation Effects Assessment Project (McCarty *et al.*, 2008).

The Choptank River watershed is similar to many of the agriculturally-dominated areas on the Delmarva Peninsula, and careful studies of this river can provide important information on the effects of land use and watershed management on water quality within the estuary. The current land use in the basin is approx-

imately 60% agriculture, 30% forest, 6% urban/residential and 4% wetlands (Fisher *et al.*, 2006a, 2006b). Primary crops in this area are corn (*Zea mays L.*), soybean (*Glycine max L.*), wheat (*Triticum aestivum L.*), and barley (*Hordeum vulgare L.*). Much of the grain

Figure 1. Map of sampling and monitoring stations and wastewater plants in the Choptank River and basin. Inset: location of the Choptank basin in the Mid-Atlantic region of the USA.



production supports small- and medium-sized animal feeding operations (mostly poultry with some dairy and horse husbandry, USDA, 2007, 2008). Manures from these operations are routinely recycled as a fertilizer for agricultural production. Several wastewater treatment plants are also located on this river (Figure 1), and a number of marinas with private and commercial boats are located in the lower estuary.

Since 1998, various segments of the Choptank River have been classified as “impaired waters” under the Federal Clean Water Act. The lower estuarine portion of the Choptank River is chronically impaired due to critically low dissolved oxygen at bottom depths, high phytoplankton content, and high nutrient concentrations (MDE, 2004), and the mouth of the Choptank River estuary has undergone an 85% decrease in the amount of area actively supporting submerged aquatic vegetation since 1997 (Orth *et al.*, 2006). The upper reaches of the estuary are well-mixed with higher dissolved oxygen concentrations, but typically exhibit elevated concentrations of nutrients and high concentrations of phytoplankton biomass (USEPA2009b). Long-term declines in water quality within the Choptank River have been documented by Fisher *et al.* (2006a). However, there are no published studies examining spatial trends in multiple contaminant types (nutrients, herbicides, metals) and water quality parameters over time in the Choptank River estuary.

Nitrogen and phosphorus have a variety of sources, including agriculture, WWTP, septic systems, non-agricultural fertilizers (lawns/golf courses), and atmospheric deposition. Although required elements for primary production, excess nitrogen and phosphorus can cause a cascade of environment effects, including algal blooms, altered phytoplankton community structure, hypoxia and fish kills (Whitall *et al.*,

2004).

Herbicides are used in a variety of applications, including on row crops. Although most current use pesticides are not as environmentally persistent as many historically used pesticides, both the parent compounds and degradation products can move into aquatic systems and have deleterious effects on estuarine organisms (Malone *et al.* 2004).

Arsenic is extremely toxic to both marine organisms and humans, and can bioaccumulate in fish, posing a threat to aquatic birds (Fujihara *et al.*, 2004). The organic arsenical compound roxarsone (3-nitro-4-hydroxyphenylarsonic acid) is commonly added to poultry feed to control coccidial intestinal parasites, thereby increasing bird growth rate. Most of the administered roxarsone is excreted into the manure as parent material (Morrison, 1969) which rapidly hydrolyzes in soil into inorganic arsenic (Stoltz *et al.*, 2007) and can end up in aquatic systems.

Although copper is an essential trace nutrient for plants and animals, at elevated concentrations copper is toxic to many organisms, especially algae and aquatic invertebrates (Kwok *et al.*, 2008). Agricultural uses of copper include application of copper sulfate and copper hydroxide as a fungicide for vegetable crops, and

Table 1. Comparison of observed data (all stations, all sampling dates) with existing water quality criteria for ecosystems (see footnotes) and methodological limits of quantification (LOQ).

Variable	Unit	Criteria	Mean	Minimum	Maximum	LOQ
Salinity	n/a	--	4.3	2.3	14	0.01
Temperature	°C	--	21.10	22.96	32.00	0.15
pH	--	--	7.51	7.50	6.79	--
Dissolved O ₂	mg/L	3.0 ^a ; 5.0 ^b	7.4	7	14.9	0.1
Nitrate + Nitrite	mg/L	None	1.28	0.79	3.97	0.01
Ammonia	mg/L	N/A ^c	0.21	0.15	1.1	0.01
Dissolved P	mg/L	None	0.07	0.05	0.36	0.01
Chlorophyll <i>a</i>	µg/L	2.6-7.6 ^d	9.0	8.1	25	0.1
TSS	mg/L	--	18	15	40	0.1
Atrazine	µg/L	10-20 ^e	0.28	0.1	1.86	0.002
Simazine	µg/L	3,700 ^f	0.24	0.07	1.89	0.002
CIAT	µg/L	--	0.14	0.10	0.64	0.002
CEAT	µg/L	--	0.12	0.05	0.80	0.002
Metolachlor	µg/L	25,000 ^g ; 3,900 ^h	0.14	0.04	1.19	0.001
MESA	µg/L	--	1.80	1.70	5.29	0.01
MOA	µg/L	--	0.39	0.35	0.89	0.01
Copper	µg/L	4.8 ⁱ ; 3.1 ^j	12.7	9.9	40.3	10
Arsenic	µg/L	69 ⁱ ; 36 ^j	0.46	0.40	1.22	0.15

^aFor no more than 12 hours, interval between excursions at least 48 hours, everywhere (USEPA, 2003)

^bAll times, throughout above-pycnocline waters (USEPA, 2003)

^cAmmonia toxicity is variable, and varies with pH and temperature (USEPA, 1999)

^dUSEPA, 2003

^eUSEPA, 2006b

^f96-h LC₅₀ for oysters (WSSA, 1994)

^g48-h EC₅₀ in *Daphnia magna* (WSSA, 1989)

^h48-h EC₅₀ aquatic invertebrates (USEPA, 1995)

ⁱAcute toxicity (USEPA, 2008b)

^jChronic toxicity (USEPA, 2008b)

as an herbicide to kill unwanted aquatic vegetation (Ex-toxnet, 2009). Copper is also used in antifouling paints to protect boat hulls from bioorganisms and has largely replaced the banned tributyltin products (Schiff *et al.*, 2003).

APPROACH

This study quantified chemical constituents that can result from anthropogenic activities, including agriculture, and several water quality indicators. The constituents included: nutrients, selected metals (As and Cu) and pesticides; and the water quality parameters were: dissolved oxygen (DO), total suspended solids (TSS) and chlorophyll a. (see Table 1). Estuarine water samples were collected from just below the water surface (0.1 m) at seven locations along the navigable portion of the Choptank River (Figure 1), using a small research vessel. Sampling dates were selected to repre-

sent base flow or near-base flow conditions in the watershed tributaries, at least two days after any significant (greater than 10 mm) rainfall event and flow less than 5 m³/s at the local USGS monitoring. Samples were collected on thirteen dates between March 2005 and April 2008; tide stage varied among sampling dates. Samples were collected, stored and analyzed in accordance with standard techniques (see Whitall *et al.* 2010 for more detailed methodology).

KEY FINDINGS

- In surface water samples collected in this study, 84% ($n = 82$) showed DO concentrations above 5 mg/L, and the remaining 12 samples had DO concentrations in the moderate range of 2 – 5 mg/L (Table 1). Concentrations showed a seasonal cycle with significantly lower ($p < 0.05$) concentrations observed

Figure 2. Box plots of nitrate-N, dissolved phosphorus, salinity, and chlorophyll a concentrations by sampling station, noting the minimum and maximum values and the median.

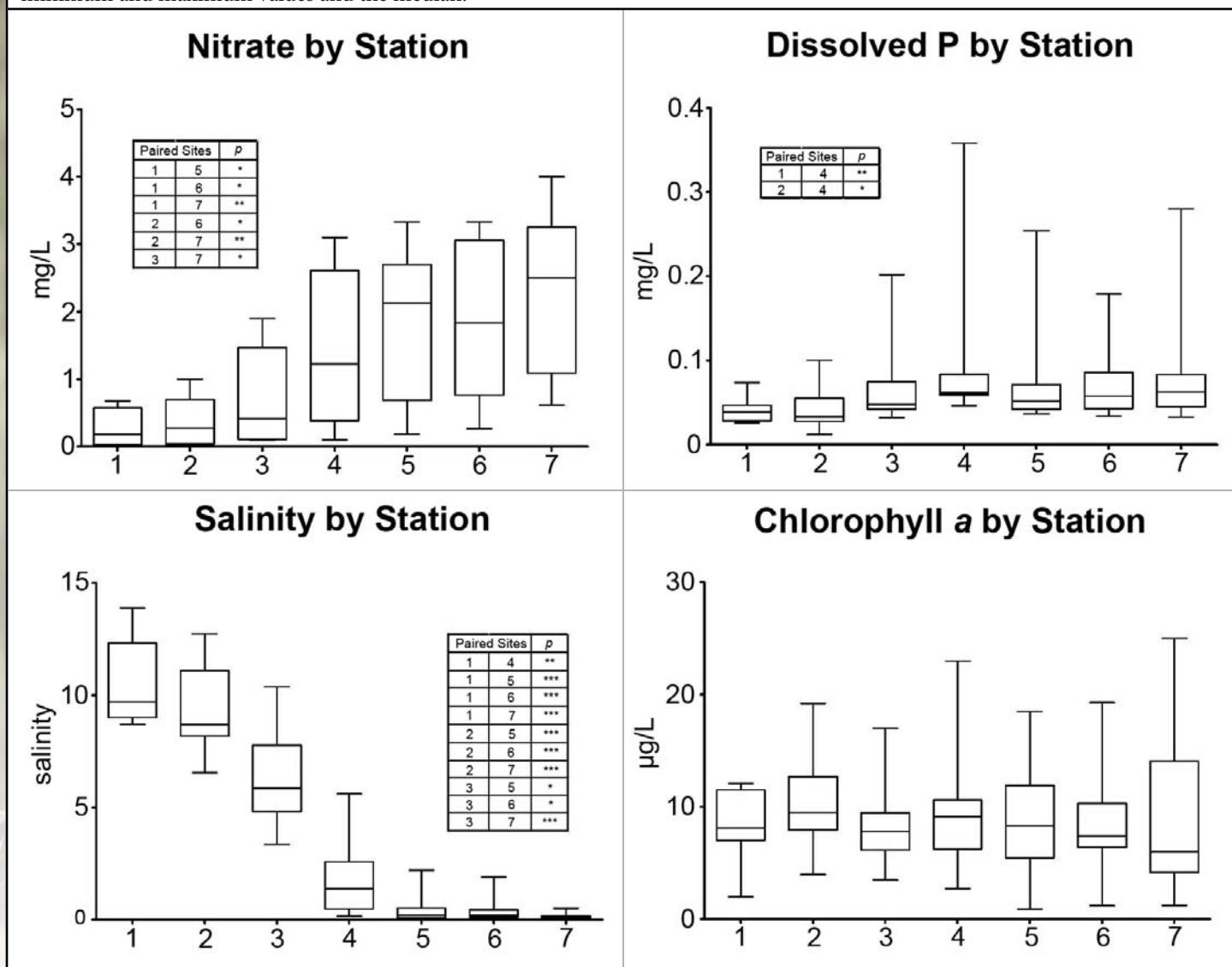
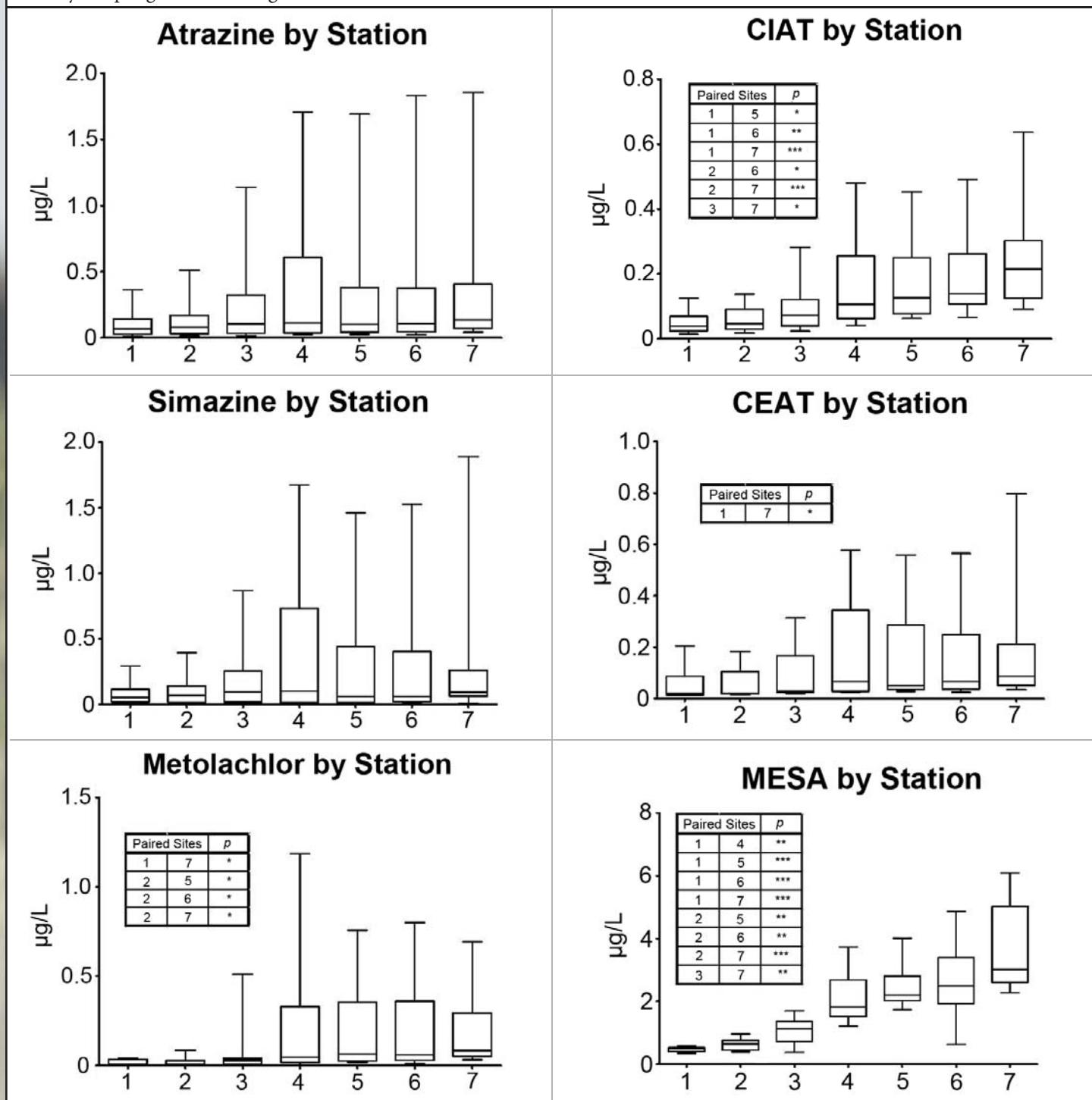


Figure 3. Box plots pesticides and their degradation products (atrazine, simazine, metolachlor, CIAT, CEAT, and MESA) concentrations by sampling station, noting the minimum and maximum values and the median.



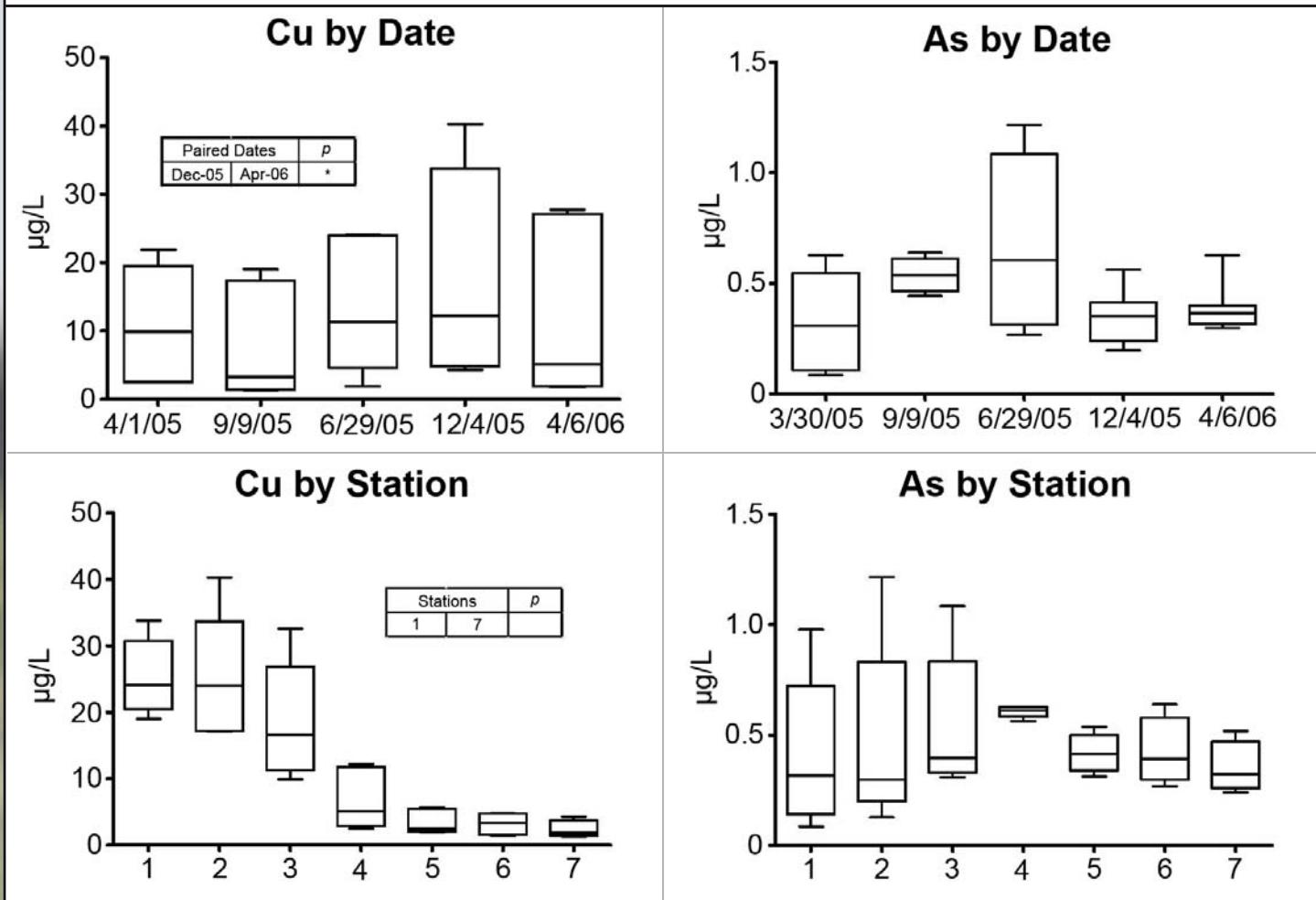
during summer months, and a negative linear correlation ($r^2 = 0.58$) observed between temperature and DO.

- Total suspended solids (TSS) concentrations ranged from 2 to 40 mg/L (Table 1), but there were not statistically significant differences between sites or significant seasonal patterns.
- Chlorophyll a content of surface waters samples

collected in this study ($n = 63$) ranged from 0.9 to 25 mg/L, with 10% of samples exceeding 16.9 $\mu\text{g/L}$ (Table 1, Figure 2), a level indicative of eutrophic conditions (USEPA, 2003). A seasonal peak was observed in the early summertime (May-July) and the maximum observed concentration of 25 $\mu\text{g/L}$.

- Observed concentrations of nitrate-N ($n = 72$) ranged from 0.01 to 4.0 mg/L, with 56% of the samples falling below 1 mg/L, 15% between 1 – 2 mg/L,

Figure 4. Box plots arsenic and copper concentrations by sampling station and by sampling date, noting the minimum and maximum values and the median.



and 29% between 2 – 4 mg/L (Table 1). There is a seasonal cycle of nitrate-N concentrations, with the lower values observed in the late summertime. Total ammonia concentrations ($\text{NH}_3 + \text{NH}_4^+$) were also detected in all samples ($n = 82$) and ranged from 0.01 to 1.10 mg/L. No significant spatial or seasonal differences were observed, although higher concentrations were typically observed in the spring and at the mouth of the river (stations 1 – 3) (Figure 2). There are currently no water quality criteria for nitrogen.

- Observed concentrations of dissolved P ranged from 0.01 to 0.36 mg/L, with 89% ($n = 73$) falling below 0.1 mg/L (Table 1, Figure 2). The highest synoptic concentrations of dissolved P (0.06 to 0.36 mg/L) were observed on July 11, 2006, following a period of heavy storm flow when 25 cm of rain fell over the course of two weeks. There are currently no water quality criteria for phosphorus.
- Herbicides and their residues were detected the

majority of samples but concentrations were generally low and did not exceed water quality standards (Table 1, Figure 3). Parent herbicide concentrations varied significantly on a temporal scale with the highest concentrations occurring during the spring application period. A smaller second peak in metolachlor concentration was observed in mid-summer (July 2006) corresponding to the herbicide application time period for double-cropped soybeans. This rapid response of receiving waters to agricultural management practices suggests that the primary delivery process for the parent herbicides to the estuary involves surface water transport rather than transport through ground water.

- Arsenic concentrations were measured during the first five sampling dates and were observed in all samples ($n = 33$). No significant differences in median arsenic concentrations were observed among stations or among sampling dates (Figure 4). All concentrations were well below the US EPA national recommended water quality criteria for both

acute and chronic exposure to estuarine organisms and were below the maximum level of concern of 10 µg/L for drinking water (USEPA, 2006a).

- Copper concentrations were measured during the first five sampling dates and were observed in all samples ($n = 33$). Median copper concentrations in this study varied significantly among sampling dates and stations (Figure 4). Spatially, the highest Cu concentrations were consistently observed in the lower portion of the estuary. These data clearly indicate that agriculture is not the primary source of Cu in the Choptank River, and that there are significant downstream sources of Cu loading to the estuary, possibly from copper released from the antifouling paints used on boat hulls, which have been shown elsewhere to contaminate waters and sediments (Warken *et al.*, 2004). The chronic and acute water quality criteria for copper are relatively low at 3.1 and 4.8 µg/L, respectively (Table 1, USEPA, 2008b). These criteria were violated for multiple sites and sampling dates in the middle and lower portions of the estuary. This exceedance of water quality criteria requires further study to determine the sources of this copper.

A more detailed discussion of these findings can be referenced in Whitall *et al.* (2010).

CONCLUSIONS

Results of this work emphasize the importance of measurement of multiple water quality parameters and contaminant concentrations to identify and understand primary water quality problems and dynamics within Chesapeake Bay tributaries and other estuaries. These resulting datasets can aid in the development of effective strategies for improving water quality and overall ecosystem health. Studies such as these provide a more realistic assessment of pollutant sources and risks, and can provide information towards adaptive management of the Chesapeake Bay and its tributaries.

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CHAPTER 8:

A Survey of Human Use Pharmaceuticals in Water Samples from the Chesapeake Bay



Anthony S. Pait^{*1}, Robert A. Warner¹, S. Ian Hartwell¹, Judd O. Nelson², Percy A. Pacheco³, and Andrew L. Mason¹

National Centers for Coastal Ocean Science, Center for Coastal Monitoring and Assessment¹

University of Maryland, College Park²

NOAA, Management and Budget, Special Projects Division³

*Corresponding author, tony.pait@noaa.gov, 301-713-3028, x158 (phone), 301-713-4384 (fax)

BACKGROUND

The assessment of emerging risks in the aquatic environment is a major concern and focus of environmental science (Daughton and Ternes, 1999). One significant class of chemicals that has received relatively little attention until recently is human use pharmaceuticals. In 2009, an estimated 3.9 billion prescriptions were written for the top 300 pharmaceuticals in the U.S. (Kaiser, 2010). The use of pharmaceuticals is also estimated to be on par with agrochemicals (Daughton and Ternes, 1999). Unlike agrochemicals (e.g., pesticides) which tend to be delivered to the environment in seasonal pulses, pharmaceuticals are continuously released through the use/excretion and disposal of these chemicals, which may produce the same exposure potential as truly persistent pollutants.

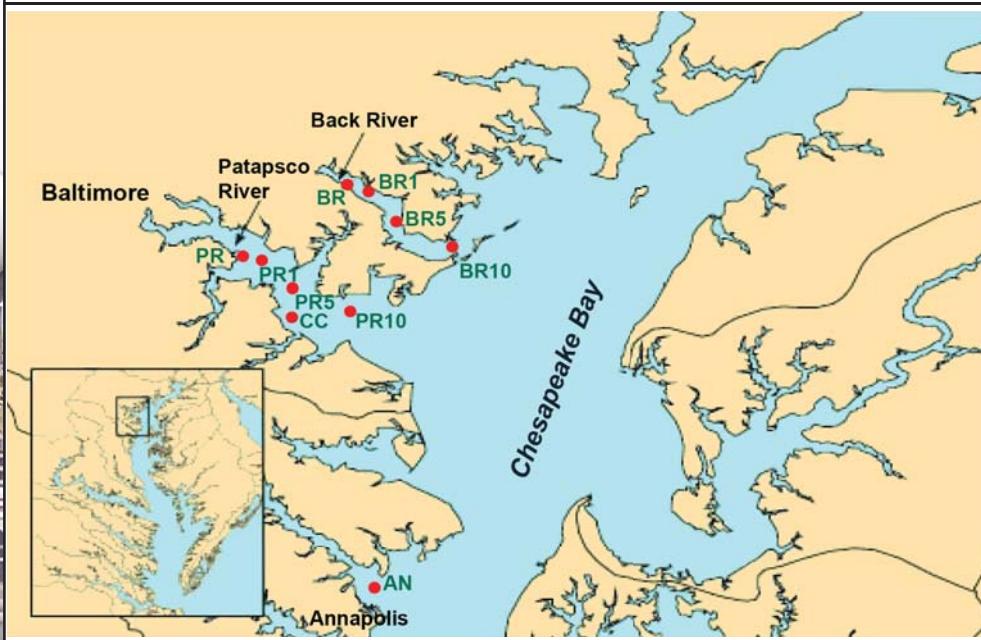
Human use pharmaceuticals can enter the aquatic environment through a number of pathways, although the main one is thought to be via ingestion and subsequent excretion by humans (Thomas and Hilton, 2004). In wastewater treatment plants (WWTPs), a number of pharmaceuticals are only partially removed by conventional biological treatments, resulting in their discharge to surface waters (Andreozzi *et al.*, 2002).

Halling-Sørensen *et al.* (1998) noted that pharmaceuticals are developed with the intention of hav-

ing a biological effect, and often have physico/chemical properties (e.g., ability to pass through membranes, persistence) chosen to avoid their inactivation prior to having a curative effect. In addition, Brain *et al.* (2004) concluded that while the concentrations of individual compounds in the environment are low, the combination of a variety of pharmaceuticals in natural waters could prove toxicologically significant. Boyd and Furlong (2002) noted that potential impacts from pharmaceuticals in the environment include abnormal physiological effects, impaired reproduction, increased cancer rates, and disruption of bacterial beds used to treat wastewater in many treatment plants. There is also concern that the continuous addition of antibiotics to the aquatic environment could result in the emergence of antibiotic-resistant, disease causing strains of bacteria (Yang and Carlson, 2004).

Andreozzi *et al.* (2003) concluded that detection of pharmaceutical residues in the environment raises questions about the impacts they may be having, and highlighted the need for data on exposure in the aquatic environment. To assess exposure, information is needed on the occurrence and concentration of these chemicals. One strategy is to look for pharmaceuticals in waters adjacent or downstream of likely points of discharge, such as WWTPs. These areas would likely

Figure 1. Northern Chesapeake Bay sampling sites.



have higher concentrations, and perhaps detectable impacts in aquatic organisms.

Currently, the Environmental Protection Agency (EPA) and the U.S. Geological Survey (USGS) are investing significant resources to assess the contamination of freshwater systems with prescription and non-prescription pharmaceuticals (Daughton and Ternes, 1999; Kolpin, *et al.*, 2002). To understand the implications in the coastal aquatic environment, NOAA's National Status and Trends (NS&T) Program within the National Centers for Coastal Ocean Science conducted a pilot study to assess the presence of a suite of human use pharmaceuticals at selected sites in the Chesapeake Bay. The NS&T Program has monitored organic and inorganic contaminants and their effects in the Nation's estuaries and coastal waters for over 20 years (NOAA, 1998). As part of this effort, NS&T also investigates the occurrence of what have become known as "emerging contaminants of concern", including pharmaceuticals, which are previously unknown or unidentified classes of contaminants that may be impacting the environment.

APPROACH

For this pilot project, water samples were collected aboard the NOAA ship FERRELL from the Chesapeake Bay and tributaries in September 2002. Sampling

sites were primarily located adjacent to WWTP outfalls. The rationale for using this approach was to create the best opportunity for detecting the pharmaceuticals of interest. Eight of the 14 sites sampled in the Chesapeake were adjacent to WWTPs, and included Back River (BR), Patapsco River (PR), Cox Point (CP) and Annapolis (AN) in the northern part of the Bay (Figure 1), and near the Virginia Initiative (VIP), Atlantic (AST), Chesapeake-Elizabeth (CEP), and Nansemond (NTP) WWTPs in the southern portion (Figure 2) of the Bay. Water samples taken at these sites were collected as close as pos-

sible to the identifiable point of discharge. In addition to sampling adjacent to the WWTP discharge points in Back River and Patapsco River, water samples were also collected 1, 5, and 10 km (i.e., BR1, BR5, BR10) downstream of these WWTP facilities (Figure 1). The goal was to assess how dilution and other physical or biological processes might affect downstream concentrations of the pharmaceuticals.

The samples were filtered and extracted at the University of Maryland using the methodology of Cahill *et al.* (2004). The extracts were then analyzed for 24 pharmaceuticals and related compounds (Table 1) by

Figure 2. Southern Chesapeake Bay sampling sites.

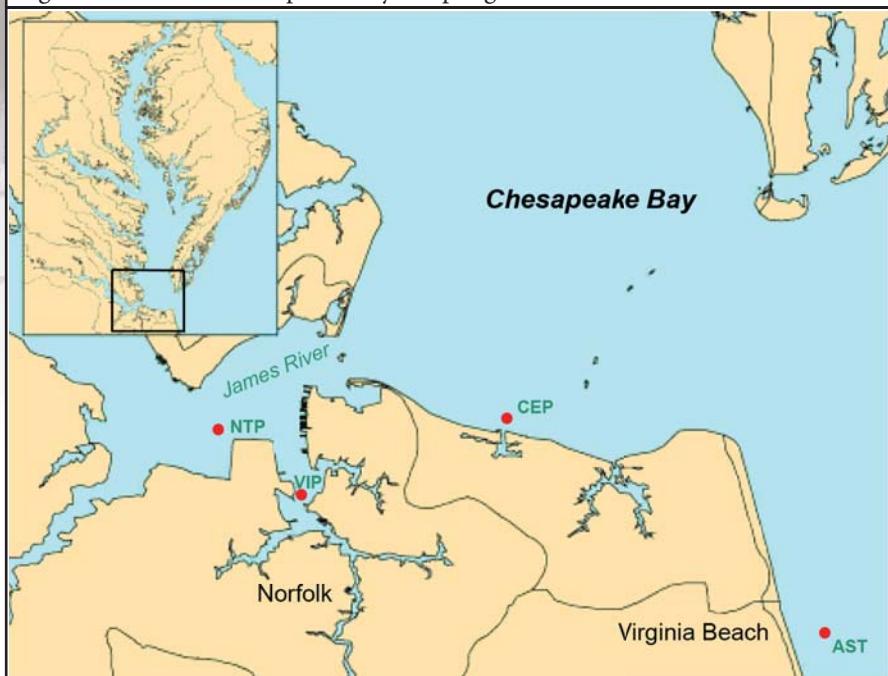


Table 1. Compounds analyzed in Chesapeake Bay water samples.

Compound	Use	Brand/Common Name	MW	CAS
1,7-dimethylxanthine	Caffeine metabolite	Paraxanthine	180.16	611-59-6
Acetaminophen	Analgesic and antipyretic	Tylenol®	151.17	103-90-2
Azithromycin	Antibiotic	Zithromax®	748.88	83905-01-5
Caffeine	Stimulant	Caffeine	194.19	58-08-2
Carbamazepine	Antiepileptic, antidepressant	Tegretol®	236.27	298-46-4
Cimetidine	Antacid	Pepcid®	252.34	51481-61-9
Codeine	Analgesic	Codeine	299.36	76-57-3
Cotinine	Nicotine metabolite	Cotinine	176.22	486-56-6
Dehydronifedipine	Antiangular	Procardia® metabolite	344.32	67035-22-7
Diltiazem	Antiangular	Cardizem®	450.98	33286-22-5
Diphenhydramine	Antihistamine	Benadryl®	291.82	147-24-0
Erythromycin	Antibiotic	E-mycin®	733.93	114-07-8
Fluoxetine	Antidepressant	Prozac®	345.8	54910-89-3
Gemfibrozil	Lipid regulator	Lopid®	250.35	25812-30-0
Ibuprofen	Analgesic and antipyretic	Motrin®	351.83	15687-27-1
Metformin	Antidiabetic	Glucophage®	129.17	657-24-9
Miconazole	Antifungal	Micatin®	416.12	22916-47-8
Paroxetine metabolite	Antidepressant	Paxil® metabolite	-	-
Ranitidine	Antacid	Zantac®	350.87	66357-35-5
Salbutamol	Antiasthmatic	Proventil®	239.3	51022-70-9
Sulfamethoxazole	Antibiotic	Bactrim®	253.28	723-46-6
Thiabendazole	Anthelmintic	Mintezol®	201.26	148-79-8
Trimethoprim	Antibiotic	Proloprim®	290.3	738-70-5
Warfarin	Anticoagulant	Coumadin®	308.33	129-06-6

Abbreviations: CAS, Chemical Abstract Service; MW, molecular weight; ®, Registered trademark

the National Water Quality Laboratory of the USGS in Denver, Colorado using high-performance liquid chromatography/mass spectroscopy (HPLC/MS) and positive mode electrospray ionization (ESI) to detect the analytes of interest.

KEY FINDINGS

- In the Chesapeake Bay, 13 of the 24 compounds analyzed were found at least once.
- The four WWTPs in the northern part of the estuary (Figure 1) had a greater average number of detected compounds (6.5) per WWTP site compared to the southern Bay (1.7). One explanation for this may be that the effluent plumes from the WWTPs near Baltimore were typically more visible and therefore samples were known to be taken in proximity of the discharge. In the southern part of the Chesapeake, there was no indication of the effluent plume, and the location of the outfalls had to be estimated using

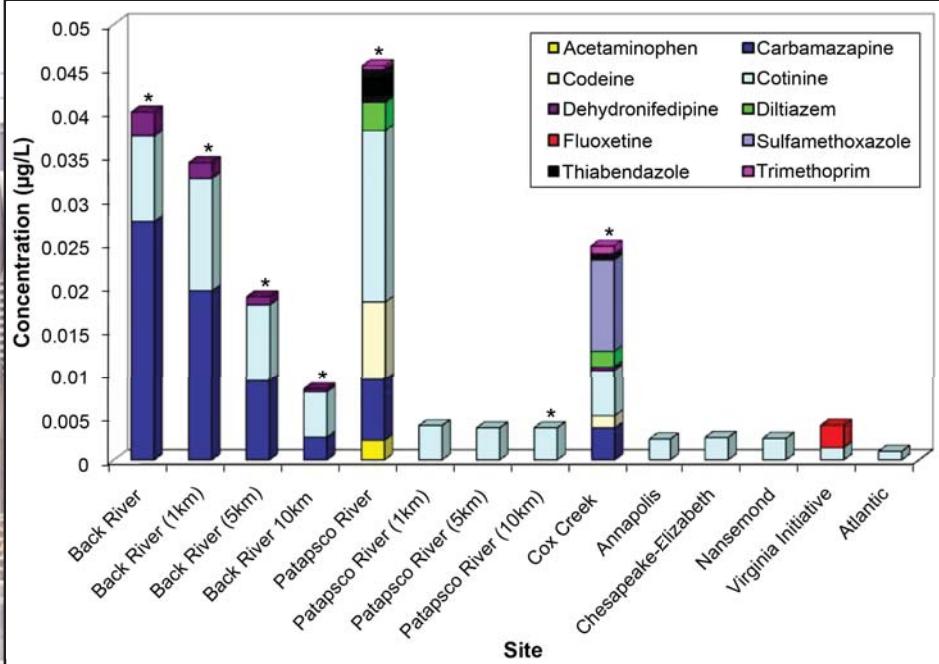
latitude and longitude coordinates.

- The most frequently detected pharmaceutical was carbamazepine, found at all sites in the northern Bay, and at one site in the southern Bay. The maximum concentration of carbamazepine was 0.030 µg/L at the outfall of the Back River WWTP. Studies have shown carbamazepine to be fairly persistent in the environment. Boyd and Furlong (2002) found carbamazepine to be one of the most frequently detected pharmaceuticals in the Las Vegas Wash, an urban river which drains the city of Las Vegas and empties into Lake Mead. Heberer (2002) found that less than 10% of carbamazepine is typically degraded during the sewage treatment process.
- Erythromycin-H₂O, a degradation product of the antibiotic erythromycin, was detected at 50% of the sites sampled in the Chesapeake Bay, including all those in the northern portion. Because of analytical difficulties (low recovery rates), detections of erythromycin-H₂O are reported rather than con-

centrations. In their assessment of pharmaceuticals and other organic contaminants in U.S. streams, Kolpin *et al.* (2002) found erythromycin- H_2O in over 21% of the water samples taken, the second highest of any antibiotic included in their inventory. Boyd and Furlong (2002) also found erythromycin in samples from the Las Vegas Wash, but not Lake Mead.

- Dehydronifedipine, a metabolite of the antianginal medication nifedipine, was found in five water samples, mainly from the Back River sites, at a maximum concentration of 0.003 $\mu\text{g/L}$. In their study of U.S. streams, Kolpin *et al.* (2002) found dehydronifedipine in approximately 14% of the samples. Boyd and Furlong (2002) also found dehydronifedipine in water samples from the Las Vegas Wash, but not from Lake Mead.
- The antibiotic trimethoprim was found twice (Patapsco River and Cox Creek) in the Chesapeake Bay samples, at a maximum concentration of 0.001 $\mu\text{g/L}$. Ashton *et al.* (2004) detected trimethoprim in 65% of WWTP effluent water samples, and 38% of downstream samples in five rivers in the U.K. Kolpin *et al.* (2002) detected trimethoprim in 27% of samples from streams in the U.S., the highest of any antibiotic included in their study.
- The antibiotic sulfamethoxazole was detected at one sampling location, Cox Creek, at a concentration of 0.011 $\mu\text{g/L}$. Kolpin *et al.* (2002) detected this antibiotic in 19% of stream samples. Boyd and Furlong (2002) detected sulfamethoxazole in both the Las Vegas Wash and in Lake Mead.
- The antidepressant fluoxetine was detected once in the southern portion of the Chesapeake Bay at a concentration of 0.003 $\mu\text{g/L}$. Kolpin *et al.* (2002) detected fluoxetine in 1% of their samples. In Louisiana, Boyd *et al.* (2003) did not detect fluoxetine in any surface water samples.
- The analgesic acetaminophen was detected at the Patapsco River site at a concentration of 0.002 $\mu\text{g/L}$.

Figure 2. Southern Chesapeake Bay sampling sites.



Ibuprofen, however, was not detected at any of the sites in the Chesapeake Bay, although it was detected in approximately 10% of the streams sampled by Kolpin *et al.* (2002).

- At the Back River and Patapsco River sites, there was evidence of a downstream (1, 5, and 10 km) concentration gradient (Figure 3). Carbamazepine, erythromycin- H_2O and dehydronifedipine were detectable in water samples 10 km downstream of the Back River. In the Patapsco River, a downstream gradient was not apparent. Interestingly, there was a detection of erythromycin- H_2O at the 10 km Patapsco River, but not at the 1 or 5 km sites. The reason for this is unknown, but could be related to discharges from the Cox Creek WWTP, which had a detection of erythromycin- H_2O , and is adjacent and somewhat upstream of the Patapsco River 10 km site (Figure 1).

CONCLUSIONS

Thirteen of the 24 compounds analyzed were found in the samples collected. The antiepileptic medication carbamazepine was detected in 11 of the 14 sites in the Chesapeake Bay. Erythromycin- H_2O was detected, but not quantified at seven sites. The effects of the pharmaceuticals in estuarine and coastal waters are currently unknown. An important first step is to document which compounds are present and at what concentrations, so that the appropriate studies (laboratory and field) can be designed to assess possible impacts.

Future work, particularly in the Chesapeake Bay is recommended to assess pharmaceuticals in both the water column and in sediments. In the Chesapeake Bay, the western shore has a higher human population, while the eastern shore is home to significant poultry CAFO (concentrated animal feeding operations) activity. A study to assess the differences in the types (human versus animal use) and concentrations of pharmaceuticals present, and a concurrent assessment of antibiotic resistant populations of bacteria in both the western and eastern shores of the Chesapeake Bay would provide information needed to begin assessing the possibility of impacts (both human and environmental) from pharmaceuticals in estuarine and coastal environments.

ACKNOWLEDGEMENTS

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POLLUTION



CHAPTER 9:

NOAA Mussel Watch Program: Chesapeake Bay



Kimbrough* Kimani, Dennis Apeti, W. Edward Johnson, and Gunnar Lauenstein

National Centers for Coastal Ocean Science,
Center for Coastal Monitoring and Assessment

*Corresponding author, kimani.kimbrough@noaa.gov, 301-713-3028 x114 (phone), 301-713-4384 (fax)

POLLUTION

BACKGROUND

NOAA's Mussel Watch Program was designed to monitor the status and trends of chemical contamination of U.S. coastal waters, including the Great Lakes. The Program began in 1986 and is one of the longest running, continuous coastal monitoring programs that is national in scope. The Program is based on yearly collection and analysis of oysters and mussels though in the Chesapeake Bay region oysters have been the sentinel species for all monitoring years. These bivalves are sessile organisms that filter and accumulate particles from water and the organisms taken from water as food; thus, measuring contaminant levels in their tissue is a good indicator of local contamination. Mussel Watch data are useful for characterizing the environmental impact of new and emerging contaminants, extreme events (hurricanes and oil spills), and for assessing the effectiveness of legislation, management decisions and remediation of coastal contamination levels.

NOAA established Mussel Watch in response to a legislative mandate under Section 202 of Title II of the Marine Protection, Research and Sanctuaries Act (MPRSA) (33 USC 1442), which called on the Secretary of Commerce to, among other activities, initiate a continuous monitoring program "to assess the health of the marine environment, including monitoring of contaminant levels in biota, sediment and the water column." As part of the NOAA Authorization Act of 1992, the overall approach and activities of NOAA's

National Status and Trends Program (NS&T), including Mussel Watch, were codified under provisions of the National Coastal Monitoring Act (Title V of the MPRSA).

In 1986, the inaugural year of the Mussel Watch Program, 145 sites were sampled. Today, Mussel Watch is comprised of nearly 300 monitoring sites nationwide while 14 sites have been established in the Chesapeake Bay region. More than 150 chemical contaminants, chosen through consultation with experts and scientists from academia and government, are measured. Many of these contaminants are listed as Environmental Protection Agency (EPA) Priority Pollutants (Keith and Teillard, 1979). Legislation has been passed to regulate most of the organic contaminants analyzed by the Mussel Watch Program. Most are toxic to aquatic organisms, and some are taken up and stored in animal tissues with the potential to be transferred through food chains to humans.

In addition to chemical contaminants, in 1995 the Mussel Watch Program began documenting histopathology conditions of oyster and mussels as further indicators of water quality. The program analyzes oysters and mussels for parasites and diseases that can impact physiological processes such as feeding, growth, spawning and even susceptibility to contaminant exposure. The program uses quantitative approaches to histopathological analysis, including the direct enumeration of parasites and the development of

Program Goal

To support ecosystem-based management through an integrated nationwide program of environmental monitoring, assessment and research to describe the status and trends of our nation's estuaries and coasts.

semi-quantitative scales for disease intensity and extent of pathological condition.

This summary for the Chesapeake Bay region brings together twenty years of Mussel Watch data on contaminant levels in oysters while results on histopathology are presented in the following chapter. This report also provides a perspective of the status and trends of chemical concentrations at the national level. In cases where no human consumption guidelines are available for shellfish, comparisons can be used to determine if the concentrations are high relative to the rest of the nation.

APPROACH

Mussels and oysters are widely distributed along the coasts, minimizing the problems inherent in comparing data from markedly different and mobile species, and making them better integrators of contaminants in a given area (Berner *et al.*, 1976; Farrington *et al.*, 1980; Farrington, 1983; and Tripp and Farrington, 1984). They are good surrogates for monitoring environmental quality because contaminant levels in their tissue respond to changes in ambient environmental levels and accumulate with little metabolic transformation (Roesijadi *et al.*, 1984; Sericano, 1993).

Because one single species of mussel or oyster is not common to all coastal regions, a variety of species are collected to gain a national perspective. A target species is identified for each site based on abundance, ease of collection and importance to local communities. Mussels (*Mytilus* species) are collected from the North Atlantic and Pacific coasts, oyster (*Crassostrea virginica*) collections range from the mid-Atlantic (Delaware Bay) southward and along the Gulf Coast, and zebra mussels (*Dreissena* species), an invasive species, are collected from sites in the Great Lakes (see figures on following pages). Oysters were the clear choice of the sentinel species for the Chesapeake Bay since they are not only good integrators of water contaminants but are also an important economic resource of the region.

Mussel Watch sites were selected to represent large coastal areas that can be used to determine the general water quality of the area associated with a monitoring site. Sites selected for monitoring are generally 10 to 100 km apart along the entire U.S. coastline, including the Great Lakes, Puerto Rico and Hawaii. Where possible, sites were selected to coincide with historical mussel and oyster monitoring locations from other programs, such as the U.S. EPA's Mussel Watch sites that were sampled from 1976 to 1978 (Goldberg *et al.*, 1983), and to complement sites sampled through state programs, such as the California Mussel Watch Program (Martin, 1985). An effort was also made to establish these monitoring sites in Marine Protected Areas such as the National Estuarine Research Reserves.

In spite of the number of sites for a coastline as large as that of the U.S., relatively few species are required to determine a national contaminant perspective. For organic contaminants it is possible to compare across all sites because Mussel Watch species have a similar ability to bioaccumulate contaminants. For trace metals there are clear differences in bioaccumulation abilities between coastal mussels and oysters. Oysters have a greater affinity for zinc, copper and silver while mussels are better able to accumulate lead and chromium.

Oysters and mussels are collected by hand or dredged from intertidal to shallow subtidal zones, brushed clean, packed in iced containers and shipped to analytical laboratories within two days of collection. Sample collection protocols are described in detail in

Mussel Watch Histopathology

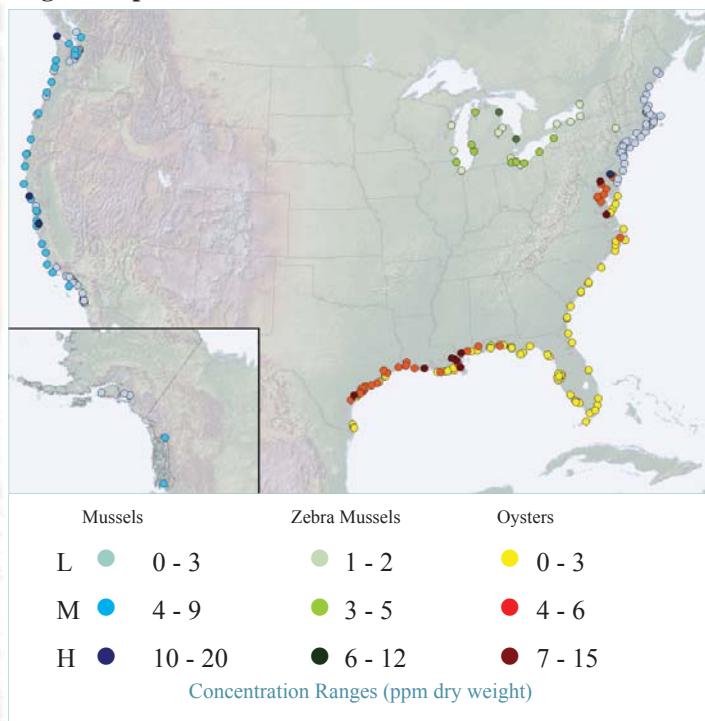


Ciliated parasites in *Crassostrea virginica*. Arrows indicate examples.

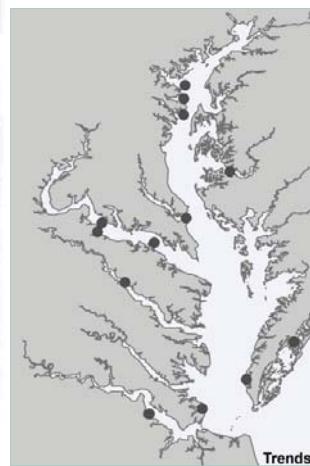
The histopathology component of the Mussel Watch Program, quantifies the stage of gamete development, and the prevalence of nearly 70 diseases and parasites found in mussels and oysters. Trends in histopathology data may help to assess the effects of global warming.

Cadmium (Cd)

Regional Species Characterization



No Trend 4

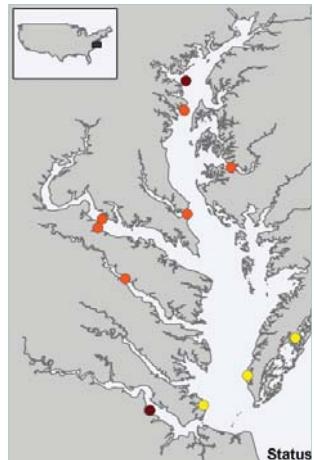


Trends

- As a region there is no cadmium trend.
- Cadmium is of a particular concern in Chesapeake Bay because, in contrast to the nation, its concentration is not decreasing despite years of restoration efforts.

Background

Cadmium is identified as a toxin of concern by the Chesapeake Bay Program. Inputs of cadmium were estimated to be 27,800 kg/year (Eskin *et al.*, 1996). The Chesapeake Bay watershed stretches across five states (NY, PA, MD, DE, VA) and the District of Columbia and is a mixed use watershed with some developed and industrialized areas. Chemical contaminant discharge into the Bay originates from industrial wastewater discharge, urban stormwater runoff, and atmospheric deposition (Chesapeake Bay Program, 1999).



Status

- The Chesapeake Bay has a much higher proportion of high and medium measurements relative to oysters nationwide.
- In comparison to the nation, the Chesapeake Bay has elevated levels of cadmium.

Site Trends



McDonald *et al.*, (2006), Lauenstein *et al.*, (1997), and Lauenstein and Cantillo (1993a-d and 1998). Sample preparation, extraction techniques and analytical methods are too voluminous to report in this document. Detailed analytical methods used by the Mussel Watch Program are available (Kimbrough and Lauenstein, 2006; Kimbrough *et al.*, 2006) online at <http://NSandT.noaa.gov>.

Along with partner laboratories, sampling and analytical methods for monitoring chemicals in

oysters, mussels and sediment have been developed. The Mussel Watch Program uses a performance based quality assurance (QA) process to ensure data quality. This effort has been in operation since 1985 and is designed to document sampling protocols, analytical procedures and laboratory performance. Analytical laboratories used by the Mussel Watch Program are required to participate in exercises with assistance from the National Institute of Standards and Technology (NIST) and the National Research Council of Canada

Regional (r)	Status (s)	Trend (t)
Oysters (O)	National Status	National Trend
4 Medium	4 Medium	G Decreasing
4 High	4 High	H Increasing

Concentrations derived from 2004-2005 data.

Markers represent the Oysters (o), National Characterization (s) and National Trends maps (t).

Site	Latitude	Longitude	General Location	Location	State
CBBO	39.1573	-76.4048	Chesapeake Bay	Bodkin Point	MD
CBHP	38.9695	-76.4147	Chesapeake Bay	Hackett Point Bar	MD
CBCP	38.6073	-76.1200	Chesapeake Bay	Choptank River	MD
CBHG	38.3123	-76.3978	Chesapeake Bay	Hog Point	MD
PRSP	38.2817	-76.9337	Potomac River	Swan Point	MD
PRMC	38.2233	-76.9615	Potomac River	Mattox Creek	VA
RRRR	37.9020	-76.7878	Rappahannock River	Ross Rock	VA
CBDP	37.0983	-76.2948	Chesapeake Bay	Dandy Point	VA
CBJR	37.0653	-76.6322	Chesapeake Bay	James River	VA
CBCC	37.2845	-76.0153	Chesapeake Bay	Cape Charles	VA
CBCI	37.9385	-75.3758	Chincoteague Bay	Chincoteague Inlet	VA
QIUB	37.5250	-75.7138	Quinby Inlet	Upshur Bay	VA

Metals (ppm)

Site	Spec	AS	o	t	CD	o	t	CU	o	t	HG	o	t	NI	o	t	PB	o	t	SN	o	t	ZN	o	t
CBBO	O	7.4			14	4		867	4		0.07			3.7	4	—	0.33			0.44	4		12000	4	
CBHP	O	7.2			6.4	4		301	4		0.03			4.7	4	—	0.24			0.25	4		4570	4	
CBCP	O	5.7			3.9	4		121			0.04			3.4	4		0.12			0			2170		
CBHG	O	6.4			4.1	4		96			0.03			3.6	4		0.22			0.11			2550		
PRSP	O	5.9			3.2	4		141			0.07			3.3	4		0.2			0			2660		
PRMC	O	5.3			4.8	4		308	4		0.05			2.8	4		0.26			0.15			3770	4	
RRRR	O	5.4			4.8	4		285	4		0.06	—		2.8	4		0.15			0			2720		
CBDP	O	9.3			1.3			77			0.11	4		1.9	4		0.67	4		0			3200		
CBJR	O	4.3		—	10	4		1460	4		0.15	4		3.8	4		0.39			0.1			8110	4	
CBCC	O	10			1.2			43			0.07			1.7	4		0.34			0			1340		
CBCI	O	10			2.6			66			0.21	4	—	2	4		0.7	4	—	0			2230		
QIUB	O	11			2.4			552	4		0.22	4		2.5	4		1.3	4	—	0			4750	4	

Organics (ppb)

Sites	Spec	Butyltins	o	t	Chlordanes	o	t	DDTs	o	t	Dieldrins	o	t	PAHs	o	t	PCBs	o	t
CBBO	O	366	4	—	12			29			6.9			481			79		—
CBHP	O	297	4		11			29			6.6			—			64		
CBCP	O	22			6			14			6.9			306			23		
CBHG	O	112	4		5.7			13			3.9			—			21		
PRSP	O	76	4		9.6			27			5.2			266			60		
PRMC	O	119	4		12			26			4.8			207			57		
RRRR	O	24			3.8			8.1			0.92			200			21		—
CBDP	O	62	4	—	9.3			34			2.9			1583	4		50		
CBJR	O	65	4	—	3.6			13			0			232			157	4	
CBCC	O	14		—	3.9			30			4.1			307		—	21		
CBCI	O	6.8			2.8			14			0.99			315			25		—
QIUB	O	6.9			0			12			0			10717	4		14		

(NRC) to ensure data are comparable in accuracy and precision (Willie, 2000; Schantz *et al.*, 2000).

KEY FINDINGS

Metals

- Two sites in the Chesapeake Bay region have elevated levels of cadmium but these sites are found in areas associated with higher levels of freshwater (Apeti *et al.*, 2009) in the upper Bay and on the James River.
- Copper patterns follow those of cadmium.
- Nickel concentrations are high for oysters in Chesapeake Bay, this may reflect the natural mineral composition of the rocks and minerals in the region (Cantillo *et al.*, 1998).
- Zinc was found to be high at the site nearest to Baltimore Harbor.
- While oysters have high levels of arsenic along the US Southeast coast, high levels for arsenic were not found in the Chesapeake Bay region.
- In general, metal concentrations in Chesapeake Bay oysters showed a static temporal trend. Relative to the national concentrations, metal concentration in oysters from Chesapeake Bay are neither increasing nor decreasing.

Organics

- Current use pesticides chlorpyrifos and endosulfan have been detected in Chesapeake Bay oysters at low levels.
- Pesticides levels in Chesapeake Bay oysters may reach higher levels than currently reported due to timing of bivalve collection which does not coincide with the peak periods of pesticide use. Oysters are collected during the winter months for the standard Mussel Watch Program sampling.
- Elevated levels of butyltins are found near urban and industrial areas.
- Most organic contaminants do not have natural sources; yet, their distributions are ubiquitous.

- Areas with the highest levels of organics are experiencing declining concentrations including: chlordanes and DDT.
- In general, organic contaminants in Chesapeake Bay oysters showed a static temporal trend. Relative to the national concentrations, concentration of organic contaminant in oyster from Chesapeake Bay are neither increasing nor decreasing.

CONCLUSIONS

Metals

- Regional concentrations are affected by both anthropogenic and natural phenomena.
- High metal concentrations are associated with urbanized and industrialized regions, regional mineralogy, and in certain instances higher metals concentrations are associated with the less saline upper reaches of the Bay or in less saline tributaries to the Bay.
- Generally urban and industrial areas represent the largest source of contaminants to the environment.
- Relative to the national Mussel Watch data, metal concentration in oysters from the Chesapeake Bay showed no particular temporal trends.

Organics

- Elevated concentrations of organic contaminants are predominantly found in urban areas at the regional level.
- Organic contaminants are higher in areas of historic use and production.

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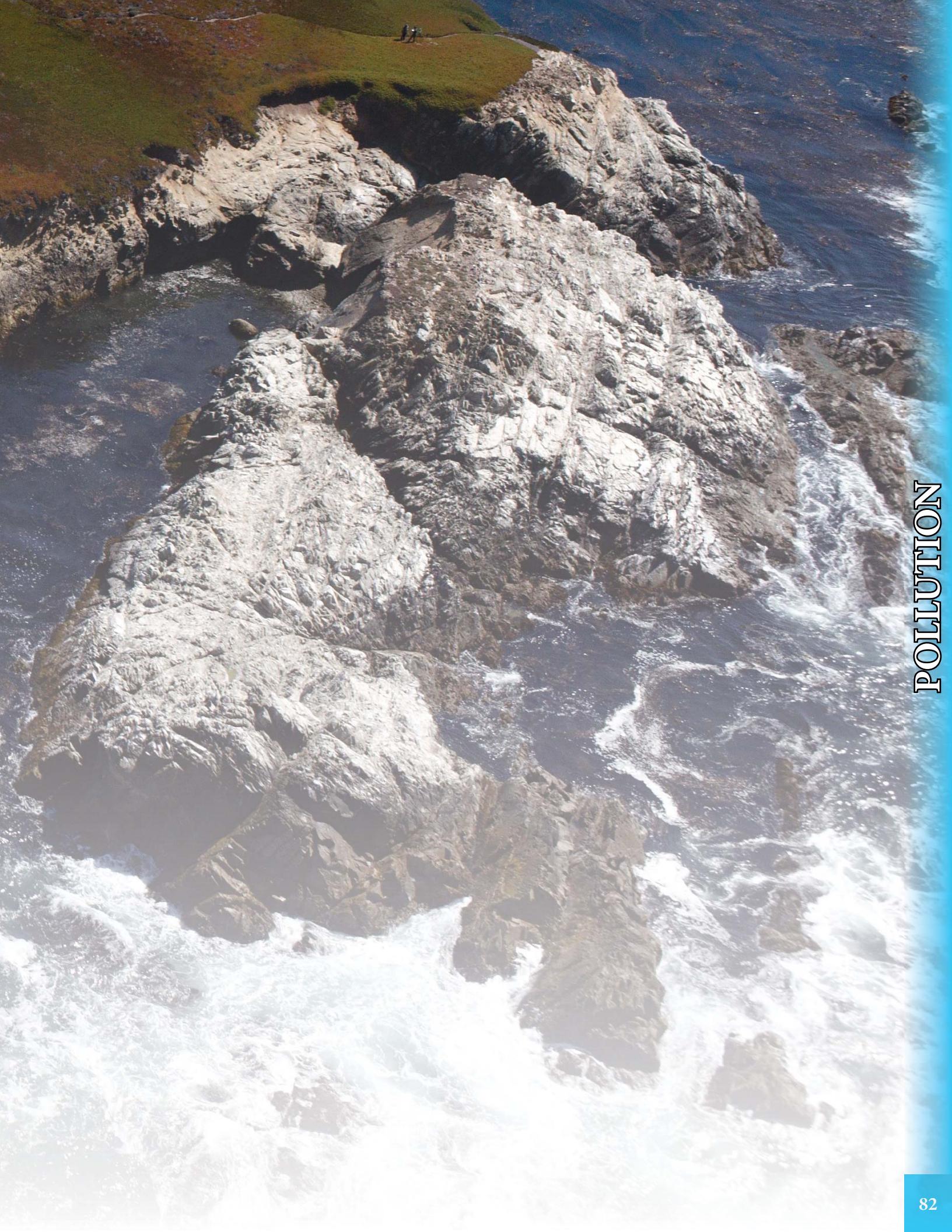
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POLLUTION



CHAPTER 10:

Occurrence of Disease and Parasites in Oysters from the Chesapeake Bay: NOAA Mussel Watch Program



Dennis A. Apeti^{*1}, Yungkul Kim², and Gunnar G. Lauenstein¹

National Centers for Coastal Ocean Science, Center for Coastal Monitoring and Assessment¹

Jackson State University²

*Corresponding author, dennis.apeti@noaa.gov, 301-713-3028, x132 (phone), 301-713-4384 (fax)

SUMMARY

The oyster population in Chesapeake Bay is currently less than one percent of historic levels. The impact this collapsing oyster fishery in the bay has regional as well as national implications. The decline of the oyster population can be attributed to many factors, including pollution, degrading water quality, overharvesting and disease. As a part of the NOAA National Status and Trends, the Mussel Watch Program monitors the health of our nation's coastal and marine waters, including Chesapeake Bay. The program documents contaminant body burdens, and the occurrence and intensity of parasites and diseases in oysters and mussels in coastal waters around the U.S. An array of about 30 parasite taxa (e.g. *Bucephalus*, *Chlamydia*, cestodes and nematodes) and 11 diseases (e.g. Dermo, MSX, tumors, neoplasm, edema and necrosis) are quantified using prevalence and intensity computation. In this document, Mussel Watch monitoring data from 1995 through 2008 were used to assess occurrence and distribution of diseases and parasites in oysters collected from 14 long-term monitoring sites in Chesapeake Bay. Correlations between diseases and parasites, and correlations between parasites/diseases and contaminant body burdens in oysters were evaluated to assess the associations among these factors and the influence of contaminants. Results indicated that gregarines, ciliates and prokaryotic inclusions were the most prevalent parasites in Chesapeake Bay. The most prevalent dis-

eases in oysters from Chesapeake Bay include Dermo, ceroid bodies, diffuse inflammation, digestive tubule atrophy, and focal inflammation. Occurrences of MSX disease, however, were infrequent. Using the infection intensity data, a number of significant correlations were observed at $p < 0.05$. For parasites, positive correlations were frequently found to occur between gregarines and MSX. Also, strong positive relationships between infection and disease intensity were observed, although gregarines vs. digestive tubule atrophy showed negative correlations. Contaminants have more significant incidents of correlations with parasites than with oyster diseases. In general, correlations between parasites/diseases and contaminants reinforce the concept that human-influenced environmental factors may affect the overall health of oysters, hence the oyster population in Chesapeake Bay.

BACKGROUND

The American or eastern oysters (*Crassostrea virginica*, Gmelin, 1791) native to the Chesapeake Bay, not only represents an important fishery with hundreds of million dollars in annual revenue (Tarnowski, 1999), but oysters are also keystone species, which play crucial ecological functions in the bay ecosystem. Oyster reefs reduce substrate erosion, induce aquatic plant stability and provide critical habitats for many marine species including small fish, crabs, worms and other invertebrates (White and Wilson, 1996). Oysters, through their

suspension feeding activities, remove particles from the water column; thereby improving water quality, which enhances photosynthesis in aquatic plants.

Estimates show that the current oyster population in Chesapeake Bay is just about 1 percent of its historic level (Chesapeake Bay Program, 2004). Evidence of the oyster population decline in the Chesapeake Bay can be shown using historical landing data. For instance, the annual commercial oyster landing in Chesapeake Bay and tributaries was an average, 2,716,568 bushels in the 1970s; 1,413,198 in the 1980s; but only 261,803 in the 1990s and 55,832 bushels in 2003 (Tarnowski, 1999). The impact of the collapsing oyster fishery in the Chesapeake Bay has regional as well as national implications. For the Atlantic Coast, the total dockside value of oysters harvest declined from \$59 million in 1992 to less than \$15 million in 2003 (NOAA restoration portal, 2010). The decline of the oyster population has been attributed to many factors, including overharvesting and habitat destruction (Rothschild *et al.* 1994); pollution and reduced water quality (Newell, 1988); disease and mortality (Tarnowski, 1999).

In 1995, the NOAA's Mussel Watch Program, which was designed to monitor the status and trends of contaminants in our coastal environments, began documenting histopathology conditions of oyster and mussels as an additional indicator of water quality. The program analyzes oysters and mussels collected from more than 300 sites around the nation for chemical contaminants, parasites and diseases that can impact physiological processes such as feeding, growth and spawning of the organisms. The program uses quantitative approaches to histopathological analysis, including the direct enumeration of parasites and the development of semiquantitative scales for disease intensity and extent of pathological condition.

This report summarizes the Mussel Watch histopathology data on Chesapeake Bay estuarine environment. In this report, Mussel Watch data were used to:

1. Evaluate the scale of occurrence of parasites and pathologies in oysters from Chesapeake Bay
2. Evaluate the scale of parasites and pathologies intensity in oysters
3. Evaluate, using prevalence data, trends in parasite diversity
4. Assess correlations between contaminant body bur-

dens and histopathology parameters (correlations with potential causative factors - parasite vs. disease and parasite/disease vs. contaminant).

METHOD

Monitoring Site and Sample Collection

The Mussel Watch Program collects bivalves biennially from a network of about 300 monitoring sites established along the U.S. coastline. In the Chesapeake Bay, oysters are collected using stainless steel dredge from 14 sites located within the geopolitical boundaries of the states of Maryland and Virginia (Figure 1). As described in detail by Lauenstein and Cantillo (1998), the standard operation procedures for Mussel Watch bivalve collection include:

- Winter collection to minimize the influence of spawning on contaminant body burdens
- Sampling targets market size animals, which may give indication of human exposure

Figure 1. Mussel Watch sites in the Chesapeake Bay region.

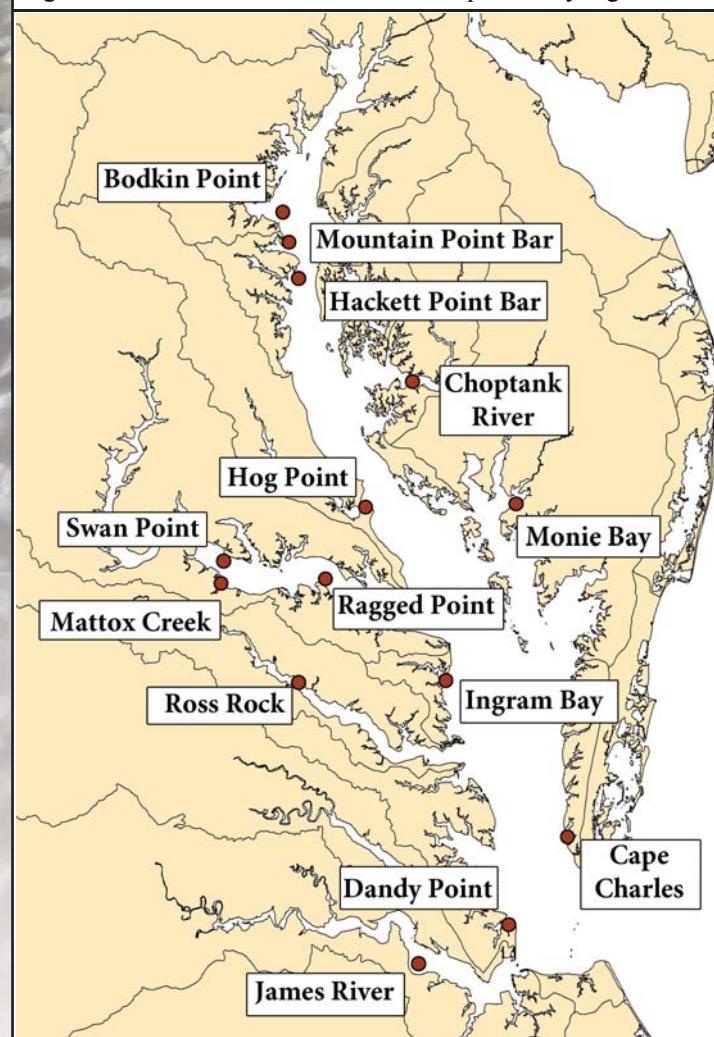


Table 1. List of parameters measured in histopathological assessment of bivalves.

Parasite		Pathology
Body cestode	Gregarine body	Ceroid bodies
Gill cestode	Gregarine gill	Diffuse inflammation
Mantle cestode	Gregarine mantle	Digestive tubule atrophy
Body copepod	Pea crab	Edema
Gill copepod	<i>Proctoeces</i>	Focal inflammation
Gut copepod	Digestive tubule protozoan	Necrosis diffuse
Digestive tract ciliate	Gut protozoan	Necrosis focal
Large gill ciliate	<i>Pseudoklossia</i>	Neoplasm
Small gill ciliate	Digestive tubule rickettsia	Tumor
Gut ciliate	Gut rickettsia	Unusual digestive tubule
Gill hydra	Nematode	Xenoma
Gill nemertine	Trematode metacercaria	Multinucleated sphere X
<i>Bucephalus</i> trematode spore	Unidentified gonoduct organism	
<i>Chlamydia</i>	Unidentified organism	Dermo infection intensity
<i>Perkinsus marinus</i>		

- Animals are kept on ice and shipped live to laboratories for analysis

Contaminants Analyzed

The Mussel Watch Program measures about 150 chemicals, including:

- Major and Trace elements – Al, Ag, Cd, Cr, Cu, Fe, Hg, Ni, Mn, Pb, Sb, Se, Sn, Zn
- PAHs - Polycyclic aromatic hydrocarbons
- PCBs - Polychlorinated biphenyls
- DDTs - dichlorodiphenyltrichloroethanes
- Dieldrins and Chlordanes - synthetic organochlorine pesticides
- Butyltins
- HCHs - hexachlorocyclohexane insecticides

Chemical analyses for the Mussel Watch Program follow stringent quality control protocols that are detailed in Kimbrough and Lauenstein (2006) and Kimbrough *et al.* (2007).

Histopathology Characterization

For the Mussel Watch Program, preparation of tissue samples for histopathological analysis follows a protocol developed at the Rutgers Haskin Shellfish Research Laboratory, Rutgers University. A detailed account of the protocol is described in the NOAA Technical Memorandum NOS NCCOS 27 (Kim *et al.* 2006). A set of quantitative and semiquantitative scales are utilized to determine the reproductive stage, and occurrence and intensity of parasites and pathologies in bivalves. Five individual organisms are randomly selected from each monitoring site and prepared for the analysis. For both gonadal index and histopathology parameters (Table 1), analyses are conducted on paraffin-embedded tissues sectioned at a 5- μm thickness using a microtome. After placing the sections onto microscope slides, the paraffin is gently removed and the tissues sections are hydrated using a xylene-ethanol series before being stained in a pentachrome series.

Each slide is examined microscopically to determine the animal's sex and stage of gonadal development. Also the infection intensity of parasites, the occurrence and extent of tissue pathologies are evaluated. Major tissue types examined include gill, mantle, gonoduct, digestive gland tubules, stomach/digestive gland and connective tissue. Parasites, diseases, or tissue pathologies are scored for intensity using either a quantitative or semi-quantitative scale, as exemplified in Table 2.

Quantitative Measures

Conditions scored quantitatively are evaluated by keeping a running count of occurrences of the condition as the slide is scanned to avoid re-examining each slide multiple times for each category. Most parasites are counted quantitatively. A number of tissue pathological conditions are also evaluated quantitatively, including the number of ceroid bodies, incidences of tissue inflammation, and tumors. Each affected area is counted.

Semiquantitative Measures

Some conditions are assigned to a semi-quantitative scale related to the intensity or the extent of the affected area (Tables 2). Definitions of scale values can be found in Kim *et al.* (2006). A semiquantitative 0-to-4-point scale is used for invasive trematode sporocysts (Fellodistomidae and Bucephalidae) based on the extensiveness of the infections. Intensity of *Perkinsus marinus* infection is also evaluated using the semiquantitative 0-to-5-point scale by Craig *et al.* (1989). MSX infection is scored on a 0-to-4-point scale of Kim *et al.* (2006) adapted from Ford and Figueras (1988). For each specimen examined, the presence of neoplasia and unusual digestive tubules is recorded. Abnormal gonadal development characterized by unusual development is given a semiquantitative 0-to-4-point score relative to the spatial coverage of the condition (Kim *et al.*, 2006). For digestive gland atrophy, a condition known to be caused by a variety of stressors most likely related to poor nutrition (Winstead, 1995), the average degree of thinning of the digestive tubule walls was assigned a numerical rating on a 0-to-4-point scale (Kim *et al.*, 2006). *Perkinsus marinus*, an oyster parasite, is also assayed semi-quantitatively but is assayed by the more precise thioglycollate method, rather than by histology (Ashton-Alcox *et al.*, 2006). Semi-quantitative measures are exemplified in this document using scales for *Haplosporidium nelsoni* (MSX) (Table 2) and digestive gland atrophy.

APPROACH

Parasite and pathological occurrences were analyzed by determining prevalence and intensity of the infections. For conditions measured semi-quantitatively,

Table 2. Semi-quantitative scale for *Haplosporidium nelsoni* (MSX) infection modified from Ford (1985, 1986) and Ford and Figueras (1988).

Score	Description
0	Uninfected, no parasites found in the tissue cross-section
1	Parasites confined to gill or digestive tract epithelial tissue, ≤ 10 plasmodia per 100X field of either gill or body tissue
2	Parasites restricted to gill or digestive tract epithelial tissue, Very light infection, $11 \leq$ plasmodia ≤ 100 per 100X field of either gill or body tissue
3	Parasites spreading into gill or digestive tract subepithelium, parasites restricted to epithelium and subepithelium area, > 100 plasmodia per 100X field of either gill or body tissue but < 1 per 1000X oil immersion field
4	Parasites more evenly distributed in gill or digestive tract subepithelium and scattered through somatic tissue, > 100 per 100X field of either gill or body tissue but 1 to ≤ 10 per 1000X oil immersion field
5	Moderate systemic infection, averaging 11 to ≤ 20 parasites per 1000X oil immersion field
6	Heavy systemic infection, averaging > 20 parasites per 1000X oil immersion field

the scale rating replaced the number of occurrences in this computation.

Prevalence describes the proportion of individuals in the population that are infected by a specific parasite or pathology and is calculated as:

$$\text{Prevalence} = \frac{\text{number of hosts with parasite or pathology}}{\text{number of hosts analyzed}}$$

Infection intensity is calculated as the average number of occurrences of the parasite or pathology in infected hosts. This is a measure of the intensity of infection in infected individuals.

$$\text{Infection intensity} = \frac{\text{total number of occurrences of parasite or pathology}}{\text{number of hosts with parasite or pathology}}$$

To evaluate the potential relationships between parasites/pathologies and contaminant body burden in oysters from Chesapeake Bay, nonparametric Spearman rank correlation test was used. Contaminant data used in this assessment include trace metals (Ag, As, Cd, Cr, Cu, Fe, Hg, Mn, Ni, Pb, Se and Zn); total organic contaminants as defined by O'Connor and Lauenstein (2006): the sum of 24 PAH compounds as total PAHs; the sum of DDT and its metabolites, DDE and DDD as total DDTs; total dieldrins as the sum of aldrin,

dieldrin, lindane and mirex; the sum of concentrations of all chlordanes as total chlordanes; and the sum of concentrations of 18 individual PCB congeners as total PCBs.

RESULTS AND DISCUSSION

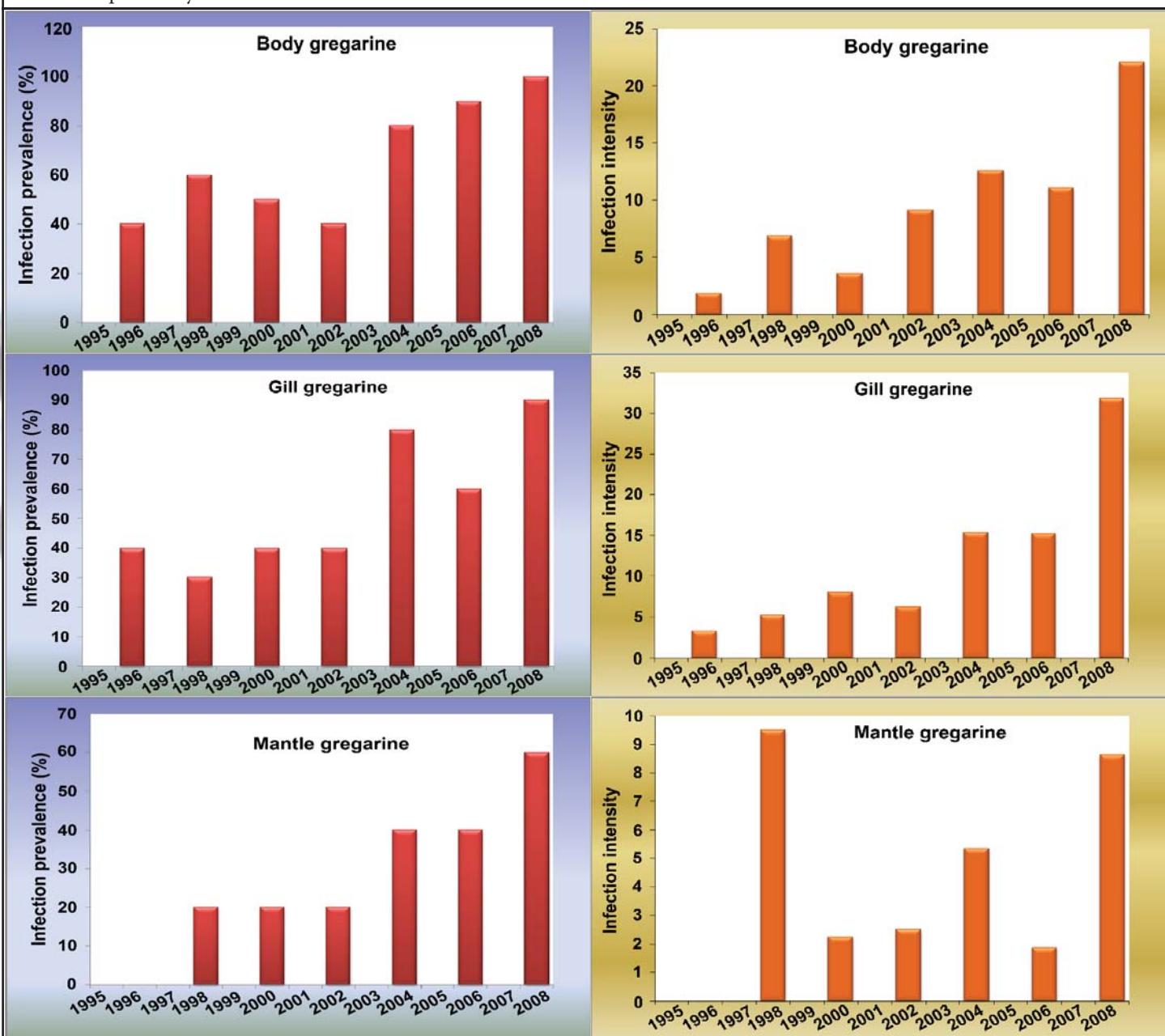
The histopathological parameters with most occurrence and high infection intensity are discussed. Among the 24 parasites, gregarine (mantle, gill and body), ciliates (gill and gut) and prokaryotic inclusions were the most prevalent in Chesapeake Bay. Among the bivalve diseases and tissue pathologies characterized by Mussel Watch, the most prevalent in oysters from Chesapeake Bay include Dermo disease, ceroid bodies, diffuse inflammation, digestive track atrophy, and focal

inflammation. Occurrences of MSX disease, however, were seldom relative to other factors. Based on the intensity data, a number of significant correlations were observed at $p < 0.05$. Among parasites and diseases, positive correlations were found between three gregarine categories and MSX. Significant correlations between contaminant body burden and parasite/disease were also observed. In Chesapeake Bay, occurrences of lethal diseases such as MSX and Dermo were more frequently correlated with metals than with organic contaminants.

PARASITES

Gregarines

Figure 2. Histogram of prevalence and infection intensity values depicting yearly occurrence of three gregarine categories in oysters from Chesapeake Bay.



- Gregarines in the genus *Nematopsis* are sporozoan parasites frequently found in oysters. Different *Nematopsis* species often show a tissue preference for either mantle or gill (Kim *et al.*, 1998).
- Mud and stone crabs are known to be final hosts (Prytherch, 1940).
- In oysters, gregarine spores typically occur in the connective tissue around the visceral mass of the body, in the gills, and in the mantle connective tissues (Kim *et al.*, 2006).

Health impact in oyster

- In general, gregarine infections are known to have low pathogenicity impact.
- However, heavy infections can cause harmful effects by physiological interferences in oysters (Sidermann, 1970).

Condition in Chesapeake Bay

- Prevalence calculations showed that gregarines (body, gill and mantle) are the most frequently observed in oysters from Chesapeake Bay with prevalence of 80 to 90 % (Figure 2).
- The Mussel Watch data showed an apparent indication of temporal increase of gregarine infection in oysters (Figure 2). This increase may be attributed to reduced water quality in the bay.
- The most frequent and heaviest infections of gregarines in Chesapeake Bay oysters occurred in 2008.
- In Chesapeake Bay gregarine infections in oysters,

were found to have strong correlations with tissue pathologies and diseases. For instance, gregarine infections were positively correlated with MSX, while they showed inverse relationships with digestive tubule atrophy (Table 3).

- Mostly, gregarine infections were inversely correlated with organic contaminant body burdens in oysters (Table 5).

Ciliates

- Generally classified as unicellular eukaryotes, ciliates are a group of protozoans characterized by the presence of hair-like organelles called cilia.
- A variety of ciliate types infect oysters from Chesapeake Bay. Ciliates occur in between gill filaments; they are also found in the gut lumen or attached to the digestive tract epithelia (Kim *et al.*, 2006).

Health impact in oyster

- Ciliate infections did not appear to elicit any obvious pathological conditions or host responses.
- No notable pathology related to ciliate infection was observed in oysters collected by Mussel Watch program (Kim *et al.*, 2006).
- Xenomas is a condition of cell expansion and damage due to multiplying ciliates. Xenoma occurrence is extremely rare in oysters from Chesapeake Bay.

Condition in Chesapeake Bay

- In Chesapeake Bay, gut ciliates occurred with low prevalences (< 40%) in oysters (Figure 3).
- Gill ciliate parasites have a very low prevalence (< 10%) and occurrences were measured only in 1998 and 2006 (Figure 3).
- Gill ciliates infections were positively correlated with infection intensities of Dermo disease in oysters (Table 3), while gut ciliate infections showed mostly inverse correlations with con-

Table 3. Significant Inter-pathology parameter correlations

parameter	parameter	Spearman	p
Gill gregarine	Body gregarine	0.982	0.000
Gill gregarine	Digest tubule atrophy	-0.768	0.002
Mantle gregarine	Body gregarine	0.880	0.000
Mantle gregarine	Digest tubule atrophy	-0.747	0.003
Digest tubule atrophy	Body gregarine	-0.777	0.002
Dermo	Gill ciliate	0.620	0.024
MSX	Body gregarine	0.591	0.034
MSX	Gill gregarine	0.633	0.020
MSX	Mantle gregarine	0.815	0.001

Table 4. Spearman correlation assessment between parasites/diseases/tissue pathology vs. metals. The data show significant correlations only.

parameter	metal	Spearman	p	parameter	metal	Spearman	p
Body gregarine	As	0.766	0.002	Gut ciliate	Ag	0.879	0.000
Body gregarine	Cd	-0.748	0.003	Gut ciliate	Cu	-0.590	0.034
Body gregarine	Fe	0.618	0.024	Gut ciliate	Hg	0.663	0.013
Body gregarine	Hg	0.829	0.000	Gut ciliate	Zn	-0.609	0.027
Body gregarine	Mn	0.627	0.022	Prokaryotic inclusion	AS	0.616	0.025
Body gregarine	Ni	-0.682	0.010	Prokaryotic inclusion	Ni	-0.658	0.014
Body gregarine	Pb	0.835	0.000	Prokaryotic inclusion	Zn	-0.625	0.022
Gill gregarine	As	0.806	0.001	Digest tubule atrophy	AS	-0.615	0.025
Gill gregarine	Cd	-0.766	0.002	Digest tubule atrophy	Cd	0.681	0.010
Gill gregarine	Fe	0.578	0.039	Digest tubule atrophy	Fe	-0.562	0.045
Gill gregarine	Hg	0.766	0.002	Digest tubule atrophy	Hg	-0.573	0.040
Gill gregarine	Mn	0.598	0.031	Digest tubule atrophy	Pb	-0.626	0.022
Gill gregarine	Ni	-0.659	0.014	Ceroid	Hg	-0.648	0.017
Gill gregarine	Pb	0.795	0.001	Dermo	Fe	0.566	0.044
Gill gregarine	Se	0.561	0.046	Dermo	Hg	0.599	0.031
Gill gregarine	Sn	-0.558	0.048	Dermo	Ni	-0.786	0.001
Mantle gregarine	Al	0.717	0.006	Dermo	Pb	0.714	0.006
Mantle gregarine	AS	0.657	0.015	MSX	Ag	0.646	0.017
Mantle gregarine	Cr	0.709	0.007	MSX	Al	0.743	0.004
Mantle gregarine	Fe	0.777	0.002	MSX	Cr	0.689	0.009
Mantle gregarine	Hg	0.818	0.001	MSX	Fe	0.676	0.011
Mantle gregarine	Mn	0.747	0.003	MSX	Mn	0.622	0.023
Mantle gregarine	Pb	0.836	0.000	MSX	Pb	0.649	0.016
Mantle gregarine	Se	0.621	0.023	MSX	Se	0.797	0.001

Table 5. Spearman correlation assessment between parasites/diseases/tissue pathology vs. organic contaminants. The data show significant correlations.

Parameter	Organic	Spearman	p	Parameter	Organic	Spearman	p
Body gregarine	Dieldrins	-0.897	0.000	Mantle gregarine	Chlordane	-0.645	0.017
Body gregarine	PCBs_18	-0.841	0.001	Gut ciliate	PCBs_18	-0.643	0.024
Body gregarine	Butyltins	-0.818	0.001	Gut ciliate	DDTs	-0.632	0.020
Body gregarine	Chlordane	-0.783	0.002	Prokaryotic inclusion	DDTs	-0.694	0.008
Body gregarine	DDTs	-0.760	0.003	Prokaryotic inclusion	Dieldrins	-0.614	0.026
Body gregarine	HCHs	-0.668	0.013	Prokaryotic inclusion	HCHs	-0.565	0.044
Gill gregarine	Dieldrins	-0.897	0.000	Prokaryotic inclusion	PAHs_24	0.587	0.035
Gill gregarine	PCBs_18	-0.863	0.000	Digest tubule atrophy	PCBs_18	0.624	0.030
Gill gregarine	Chlordane	-0.806	0.001	Digest tubule atrophy	DDTs	0.657	0.015
Gill gregarine	Butyltins	-0.777	0.002	Digest tubule atrophy	Chlordane	0.659	0.014
Gill gregarine	DDTs	-0.777	0.002	Digest tubule atrophy	Dieldrins	0.702	0.007
Gill gregarine	HCHs	-0.708	0.007	Digest tubule atrophy	HCHs	0.717	0.006
Mantle gregarine	Butyltins	-0.771	0.002	Ceroid	Butyltins	0.588	0.035
Mantle gregarine	Dieldrins	-0.757	0.003	Ceroid	Chlordane	0.632	0.021
Mantle gregarine	PCBs_18	-0.713	0.009	Ceroid	Dieldrins	0.680	0.011
Mantle gregarine	DDTs	-0.645	0.017	MSX	Butyltins	-0.619	0.024

taminant body burdens (Tables 4 and 5).

PATHOLOGY AND DISEASES

Dermo Disease

- The etiological agent of Dermo disease is pathogen *Perkinsus marinus*.
- Perkinsus marinus* is the most widespread pathogen of East and Gulf coast oysters (Kim *et al.*, 2006).
- Perkinsus marinus* phylogenetic placement remains controversial: it was considered a form of fungus (Mackin *et al.*, 1950), then a protozoan parasite (Levine, 1978) and dinoflagellate (Reece *et al.*, 1997).

Health impact in oyster

- Dermo is transmitted from oyster to oyster and causes significant mortalities in oyster populations (Kim *et al.*, 2006).
- Dermo disease is the major cause of oyster mortality in Chesapeake Bay, and because of the devas-

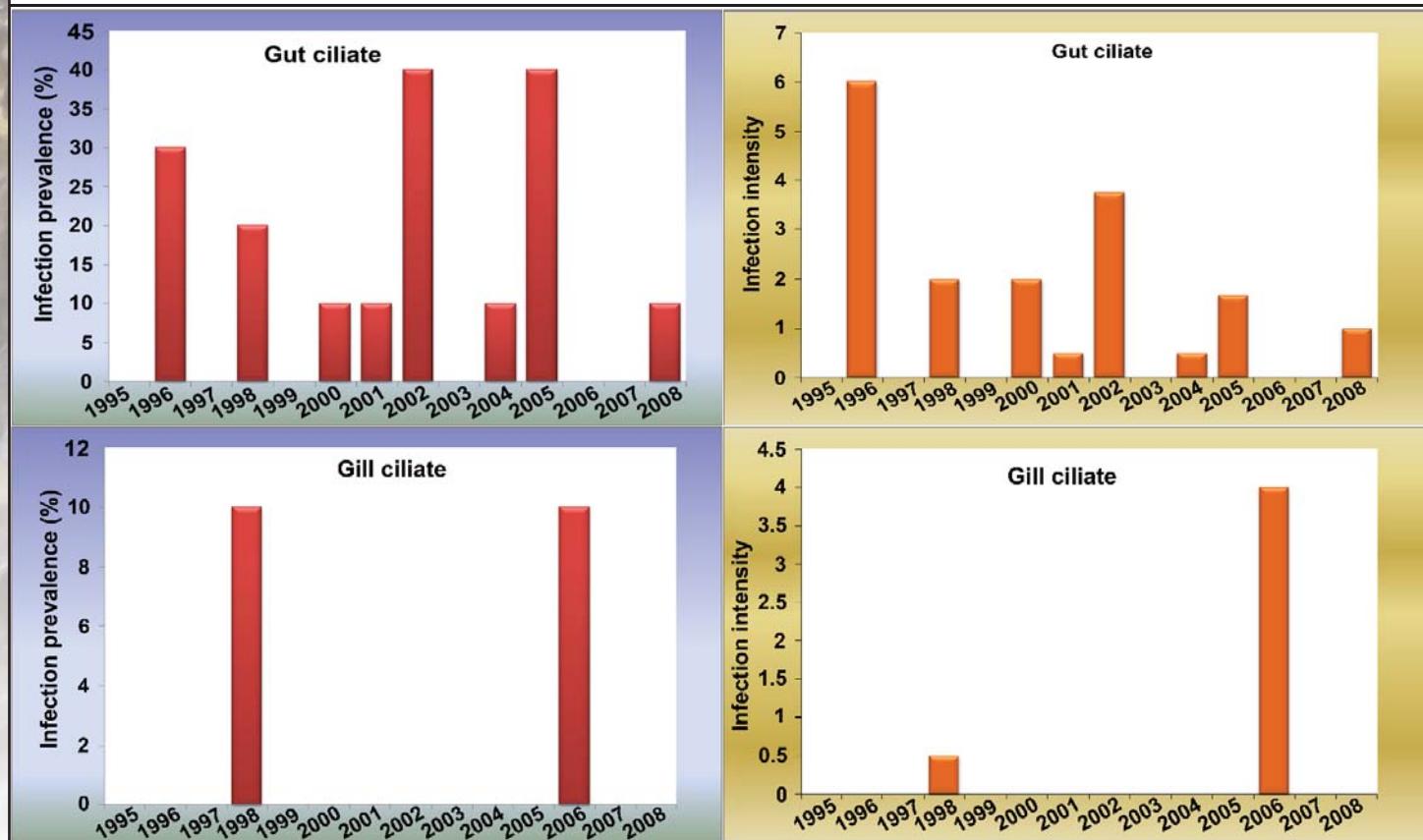
tation caused by the disease, it is recognized by the Chesapeake Bay Program as the major challenge to the oyster restoration effort in bay (Chesapeake Bay Program, 2005).

- Dermo disease has a possible link with *Vibrio vulnificus*, an important source of infection in susceptible humans eating raw oysters (Tall *et al.*, 1999 and Shapiro *et al.*, 1998).

Condition in Chesapeake Bay

- Dermo disease appeared to occur with relatively high prevalence (80 to 95 %) in Chesapeake Bay (Figure 4).
- Except for few years, occurrence of Dermo disease in Chesapeake Bay appeared to be relatively constant over the monitoring years (Figure 4).
- The highest Dermo disease intensity in Chesapeake Bay occurred in 1996, 1998 and 2006.
- In addition to a positive relationship with gill ciliates (Table 3), occurrences of Dermo disease were

Figure 3. Histogram of prevalence and infection intensity values depicting yearly occurrence of two types of ciliate infection in oysters from Chesapeake Bay.



strongly correlated with body burdens of several metals such as Hg, Pb, and Fe (Table 4).

Multinucleated Sphere X (MSX) Disease

- MSX stands for multinucleated sphere unknown or X.
- The haplosporidian protozoan, *Haplosporidium nelsoni*, is the etiological agent of MSX disease in oysters.

Health impact in oyster

- Haplosporidium nelsoni* infections start in the gill epithelium and remain in this area at light infection levels. As the disease worsens, it becomes systemic and attacks the visceral mass in heavy infection.
- MSX disease, especially heavy infections, is associated with host hemocyte infiltration into the site of infection and tissue necrosis. According to the Chesapeake Bay Program, MSX is one of the major biological stressors that cause the highest oyster mortality in Chesapeake Bay (Chesapeake Bay Program, 2004).

Condition in Chesapeake Bay

- Prevalence results indicated that MSX disease does not occur with high frequency in Chesapeake Bay.
- Infection prevalences in oysters are low with < 10% (Figure 5).
- Infection intensity showed an apparent decrease in the bay over the 1995 – 2008 monitoring period.

- In addition to a positive relationships with gregarine infections (Table 3), infection intensities of MSX disease were positively correlated with body burdens of several metals and organic contaminants such as Ag, Cr, Fe, Mn, Se and butyltins (Tables 4 and 5).

Tissue Inflammation

- Tissue inflammation is characterized by intense cellular infiltration of hemocytes.
- Two types of inflammations, diffuse and focal, occur in oysters. Diffuse inflammation is distinguished from focal inflammation when hemocytes are distributed broadly over a large section of tissue without a clear center or focal point of highest hemocyte concentration (Kim *et al.*, 2006).

Health impact in oysters

- In Mussel Watch Chesapeake oyster samples, most tissue inflammation, characterized by hemocytic infiltration, and most tissue necrosis, characterized by death or decay of cells and tissues, are observed in the visceral connective tissue and is sometimes associated with the presence of parasites.
- The type of affected tissue and type of irritation responsible influence the nature of the cellular response (Ford and Tripp, 1996).

Condition in Chesapeake Bay

- The condition of tissue inflammation was commonly observed in oysters from Chesapeake Bay

Figure 4. Histogram of prevalence and intensity values depicting yearly occurrence of Dermo disease in oysters from Chesapeake Bay.

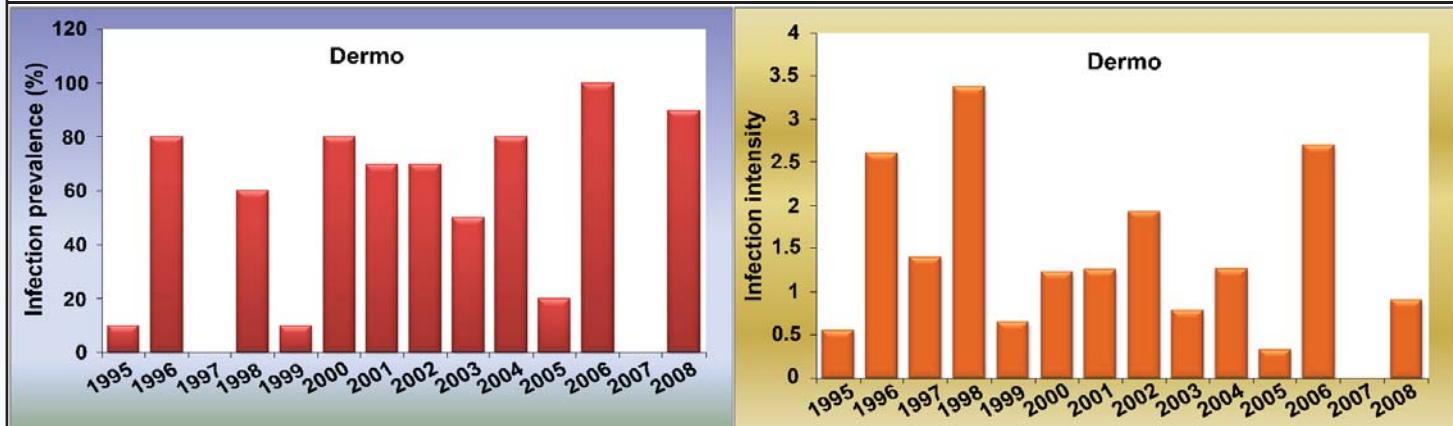
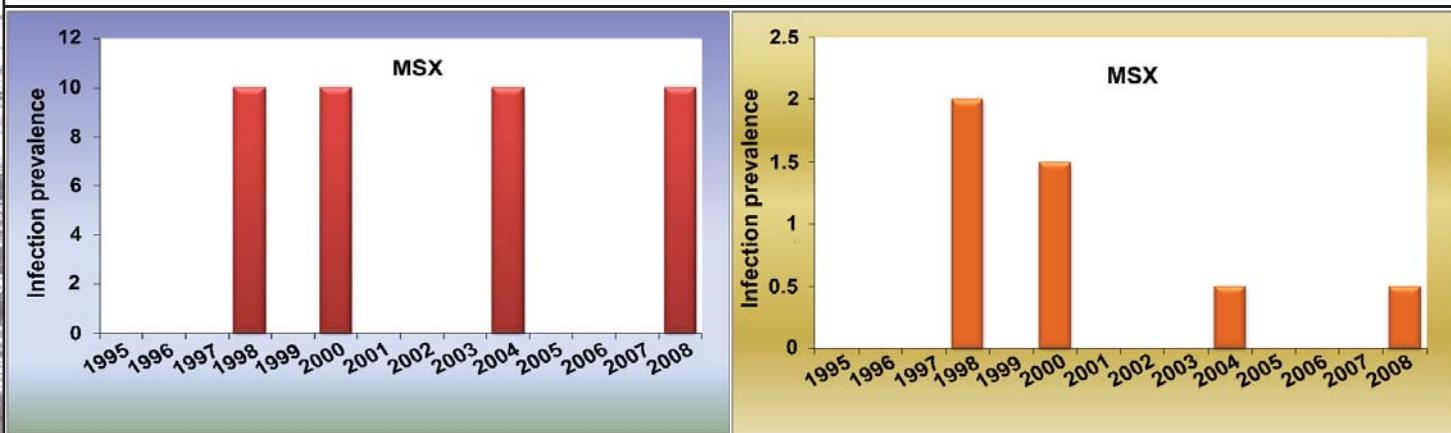


Figure 5. Histogram of prevalence and intensity values depicting yearly occurrence of MSX disease in oysters from Chesapeake Bay.



throughout the 1995 – 2008 Mussel Watch monitoring period (Figure 6).

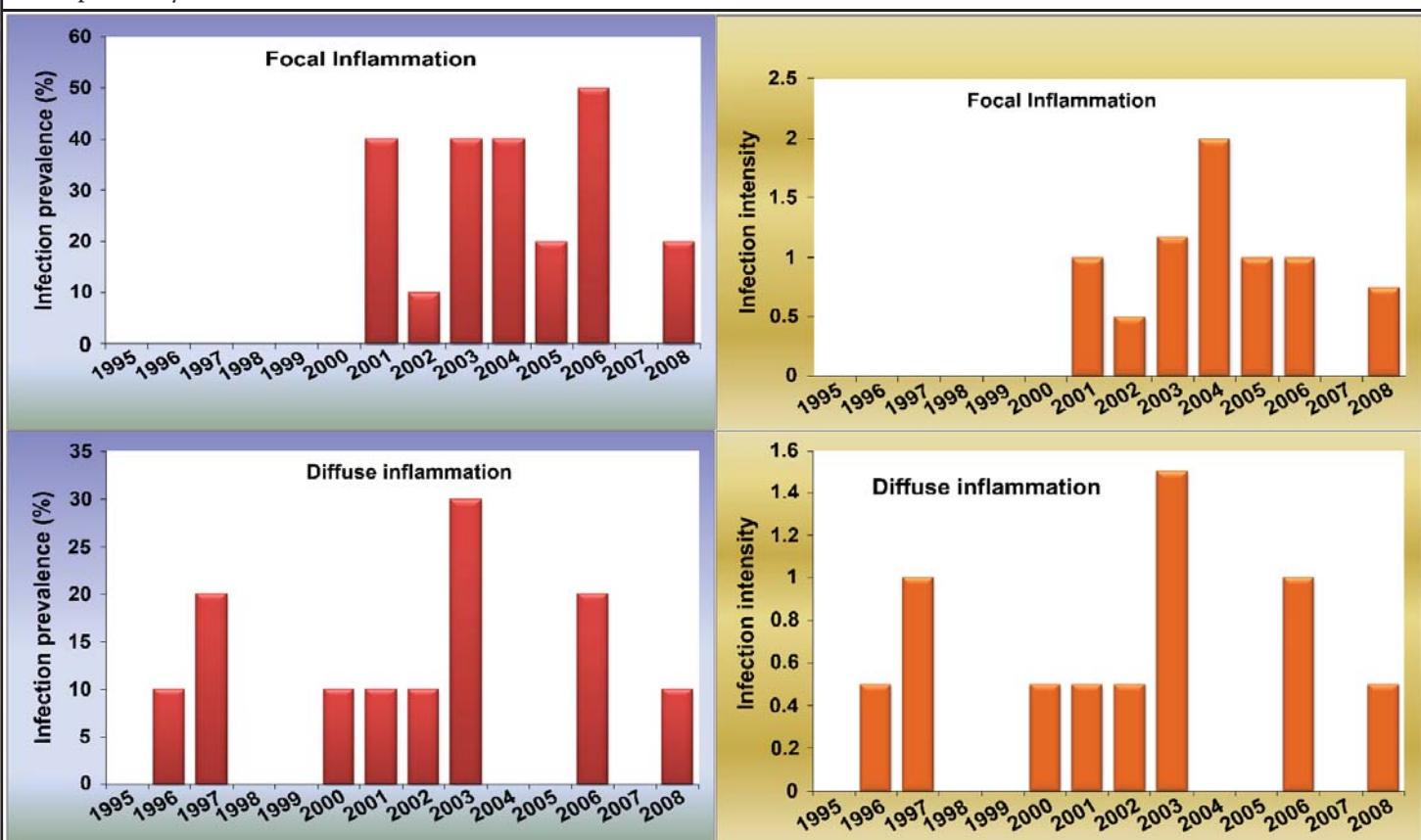
- Tissue inflammation appeared to be relatively moderate, with infection prevalence ranging between 10% to 50% and 10% to 30% for focal and diffuse inflammations, respectively.
- Incidents of the most intense cases of tissue inflammation in oysters from Chesapeake Bay occurred during 2003 – 2006.

- No significant relationship between tissue inflammations and biological parameters were observed. The same is true between tissue inflammations and chemical contaminants body burdens.

Digestive Tubule Atrophy

- This atrophy is a condition characterized by the thinning of the digestive tubule walls, which has been observed in many bivalve species.
- The occurrence of the condition has been linked to

Figure 6. Histogram of prevalence and intensity values depicting yearly occurrence of tissue inflammation conditions in oysters from Chesapeake Bay.



a variety of stressors including exposure to contaminants and poor nutrition (Winstead, 1995).

Health impact in oyster

- The digestive tubule atrophy is not necessarily a pathology.
- The condition is an abnormal organ structure that may have serious impacts on oyster growth, hence reproduction.

Condition in Chesapeake Bay

- The condition appeared to be very prominent in oysters from Chesapeake Bay.
- Prevalence was almost 100% in every monitoring year, suggesting the condition occurred in as many oysters in Chesapeake Bay (Figure 7).
- Results showed that the condition constantly occurred with relatively high severity in the Bay.

- Occurrences of digestive tubule atrophy condition were negatively correlated with gregarine parasites (Table 3) and metals (Table 4). However, the condition was positively correlated with body burdens of organic contaminants such as DDTs, PCBs, HCHs, chlordanes and dieldrins (Table 5).

Ceroid Bodies

Ceroid bodies are brown-yellow aggregates that are linked to metabolite accumulation and detoxification in oysters (Zaroogian and Yevich, 1993).

Health impact in oyster

- Ceroid bodies are a metabolic disease caused by the lack of an enzyme, which allows a waste product (ceroid lipofuscin) to accumulate in body cells.
- The condition may interfere with normal cell function.

Figure 7. Histogram of prevalence and intensity values depicting yearly occurrence of digestive gland atrophy conditions in oysters from Chesapeake Bay.

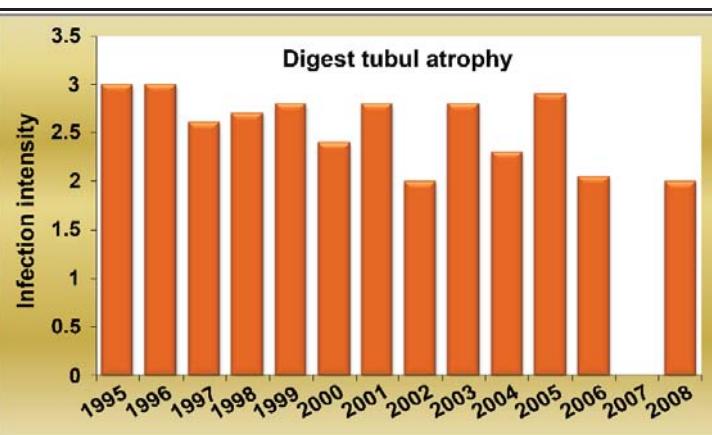
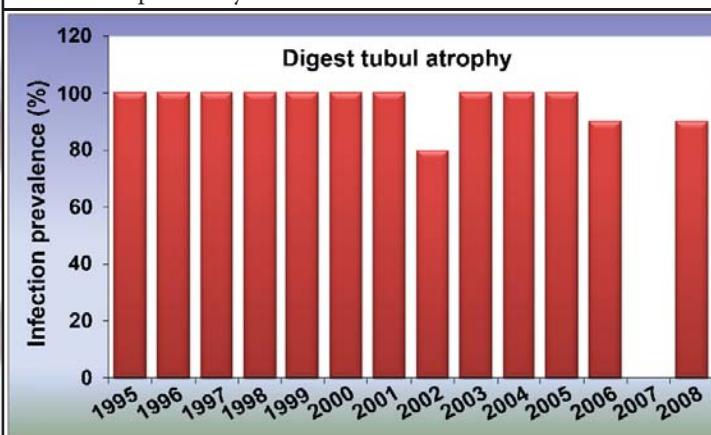
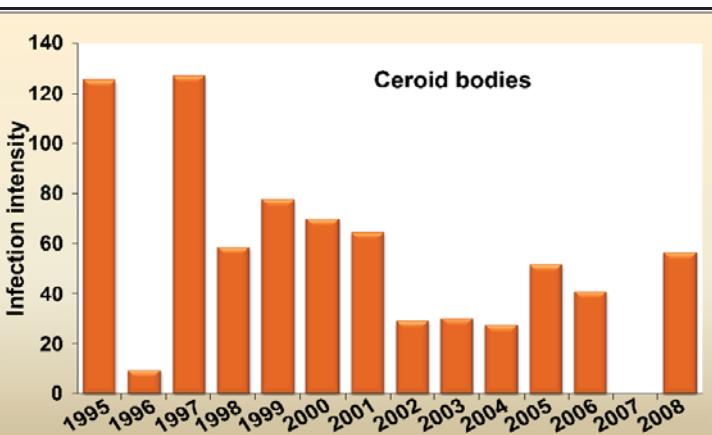
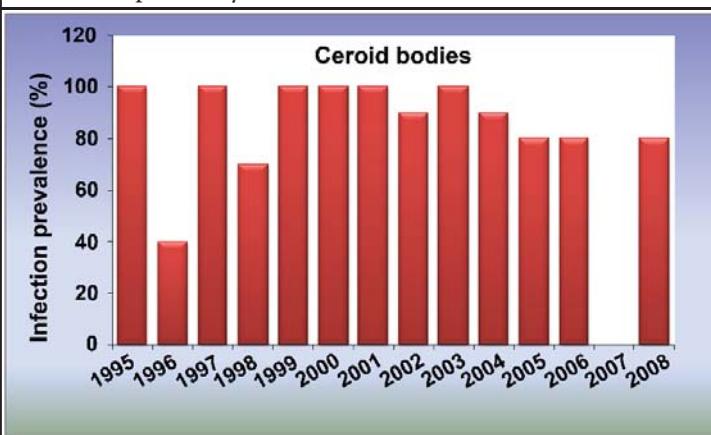


Figure 8. Histogram of prevalence and infection intensity values depicting yearly occurrence of ceroid metabolic bodies in oysters from Chesapeake Bay.



Condition in Chesapeake Bay

- The condition was frequent in oysters from Chesapeake Bay.
- In Chesapeake Bay, infection prevalences frequently reached 100% in most years (Figure 8).
- Highest abundances were recorded in 1995 and 1997.
- Ceroid bodies were positively correlated with organic contaminants such as butyltins, chlordanes and dieldrins (Table 5).

CONCLUSION

- The degree of occurrence of parasites and pathologies in oysters from Chesapeake Bay was evaluated using the National Status and Trends Mussel Watch monitoring data from 1995 to 2008.
- Among the 24 parasites, gregarines (mantle, gill and body), ciliates (gill and gut) and prokaryotic inclusions were the most prevalent groups. Among the 11 bivalve diseases and tissue pathologies, the most prevalent ones in oysters from Chesapeake Bay, include Dermo disease, ceroid bodies, digestive tubule atrophy, and tissue inflammations.
- The occurrence of one of the most harmful parasites to oysters, such as *Haplosporidium nelsoni*, which causes lethal MSX disease was less frequent.
- In contrast, *Perkinsus marinus*, which is responsible for Dermo disease, appeared frequently in Chesapeake Bay.
- Correlations between biological parameters and contaminant body burdens were assessed. A number of significant relationships between pairs of biological parameters were obtained. Although some relationships were negative, contaminant body burdens of metals were found to be positively correlated with biological parameters. Gregarines were associated with about half of the significant correlations found with metals and with organic contaminants, respectively. The two major oyster diseases, Dermo and MSX, were positively correlated with contaminants except for two cases (i.e. Dermo and Ni; MSX and

butyltins). Digestive tubule atrophy showed positive relationships with organic contaminants, but negative correlations with metals, except Cd.

- Although occurrences of parasites and diseases may have impact on oyster recruitment, growth and mortality, drastic reduction of the oyster population in Chesapeake Bay is more likely due to other factors including overharvesting, habitat destruction, pollution and reduced water quality.

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Chesapeake Bay Pathogen Monitoring and Forecasting Program: Predicting the distribution of *Vibrio vulnificus* in Chesapeake Bay



John Jacobs*, Matt Rhodes, A.K. Leight, and Bob Wood.

National Centers for Coastal Ocean Science,
Center for Coastal Environmental Health and Biomolecular Research, Cooperative Oxford Laboratory

*Corresponding author, john.jacobs@noaa.gov, 410-226-5193 (phone), 410-226-5925 (fax)

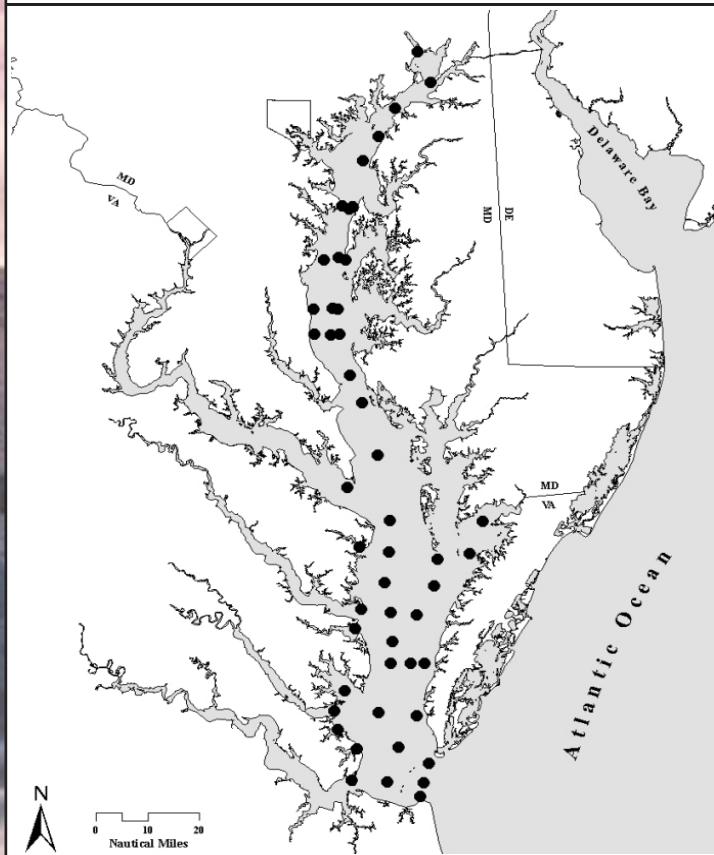
BACKGROUND

Since 2005, NOAA's Cooperative Oxford Laboratory has been working with federal, state, and academic partners to: 1) monitor potentially pathogenic species of bacteria in the Chesapeake region, 2) determine environmental factors which govern their distribution, 3) develop models and forecasts for use by public health officials, and 4) understand implications for human and living resource health (Jacobs *et al.* 2009a, Jacobs *et al.* 2009b, Jacobs *et al.* 2009c, Jacobs *et al.* 2009d, Stine *et al.* 2009, Jacobs *et al.* 2010, Matsche *et al.* 2010). Of particular concern are estuarine bacteria of the genus *Vibrio* spp. due to the potential of several species to cause severe and occasionally life threatening infections in humans. *Vibrio vulnificus* is responsible for 95% of all seafood related mortalities in the United States (Oliver & Kaper 2001). Primary septicemia associated with seafood consumption and wound infections are the most common type of *V. vulnificus* infection in humans, with gastroenteritis occurring relatively infrequently (Strom & Paranpype 2000). Cases which become septic have as high as a 50% mortality rate (Rippey 1994, Oliver & Kaper 2001). Previous reports by the Centers for Disease Control and Prevention estimated *V. vulnificus* infections annually at 97 total cases in the United States, with 48 associated deaths (Mead *et al.* 2000). Thus, it is extremely important to understand the ecology, abundance, and distribution of *V. vulnificus* in the interest of human health.

Several efforts have attempted to examine correlations of abundance or presence of *V. vulnificus* with environmental factors (O'Neill *et al.* 1992, Wright *et al.* 1996, Lipp *et al.* 2001, Heidelberg *et al.* 2002, Pfeffer *et al.* 2003, Randa *et al.* 2004). While various parameters have been reported as being correlated to *V. vulnificus* abundance, water temperature, and to a lesser extent salinity, are consistently identified variables. In general, growth and abundance are positively correlated with water temperature when greater than 15° C. Salinity may also govern abundance, but the relationship is not as clear. Several researchers have reported estuarine waters of 10-15 ppt to be the preferred salinity for *V. vulnificus* (Lipp *et al.* 2001, Randa *et al.* 2004). However, it has been cultured from higher salinity waters as well (Tamplin *et al.* 1982, Oliver *et al.* 1983) although results regarding survival and growth have been contradictory (Randa *et al.* 2004). The inconsistencies seen in the response of *V. vulnificus* to salinity gradients may result from regional and strain differences between these various studies.

Increasingly, efforts are focusing on the development and application of empirical habitat models of organisms in support of environmental forecasting (Decker *et al.* 2007, Jacobs *et al.* 2009a, Constantin de Magny *et al.* 2010). In the Chesapeake Bay, the Chesapeake Bay Ecological Prediction System (CBEPS) is being developed and implemented by scientists at the National Oceanic and Atmospheric Administration

Figure 1. Main-stem Chesapeake Bay monitoring stations used for the development of the *V. vulnificus* empirical model.



(NOAA), the University of Maryland system, the Chesapeake Research Consortium, and the Maryland Department of Natural Resources (MD DNR). The CBEPS generates Bay-wide nowcasts and three-day forecasts of several environmental variables, including temperature and salinity (Brown *et al.* 2002). In simulation, these environmental variables can be used to drive empirical habitat models of target organisms to make first order predictions of their likelihood of occurrence. Here we describe a predictive model developed for estimating the likelihood of *V. vulnificus* presence in Chesapeake Bay and demonstrate its application within the CBEPS.

APPROACH

Surface water samples (0.5-1m depth) were collected by the Maryland Department of Natural Resources and Virginia Department of Environmental Quality's respective water quality monitoring programs according to Chesapeake Bay Program protocols (USEPA 1996). Physical parameters are measured in-situ with a YSI datasonde (YSI Incorporated, Yellow Springs, Ohio, USA) and nutrient and chlorophyll analysis conducted analytically according to established protocols. Samples used for model development were collected along the mainstem of the Bay during the months of July and

October of 2007, and April, July, and October of 2008 and 2009 ($n = 235$) (Figure 1). DNA was extracted from water samples using direct filtration and protocols previously established (Jacobs *et al.* 2009a). *V. vulnificus* were enumerated using quantitative PCR (Panicker *et al.* 2004, Panicker & Bej 2005) and compared directly to the associated water quality data. Empirical models were developed and tested using logistic regression analysis to determine which water quality variables provided the greatest power in predicting *V. vulnificus* presence/absence. Finally, ChesROMS, (<http://ches.communitymodeling.org/models/ChesROMS/index.php>), a regional adaptation of the Rutgers Ocean Modeling System, was used to force empirical models derived from these large data sets.

KEY FINDINGS

- *Vibrio vulnificus* occurs most often in a narrow salinity range (~10-15ppt) and is most prevalent at elevated water temperatures ($> 15^{\circ}\text{C}$).
- The combination of water temperature and salinity can correctly classify presence of *V. vulnificus* 93% of the time in Chesapeake Bay (Figure 2).
- ChesRoms allows for 3-day forecast development.
- Hindcasting efforts suggest climate variability (wet-cool years vs. warm-dry) is expected to play a major

Figure 2. Logit model using temperature and salinity to predict the probability of occurrence of *V. vulnificus* in Chesapeake Bay.

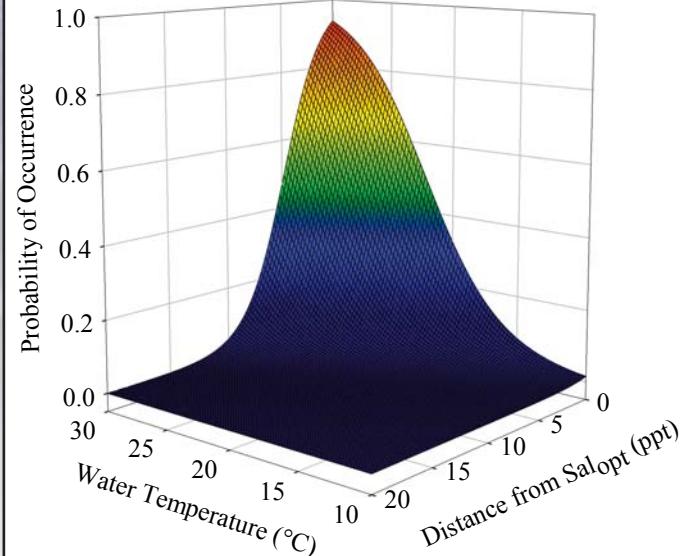


Figure 3. Hindcast depicting probability of occurrence of *V. vulnificus* in wet (1996) and dry (1999) years. Both figures represent conditions present on August 1st of each year. Color scale represents probability of occurrence with red high (100%) and blue low (0%)

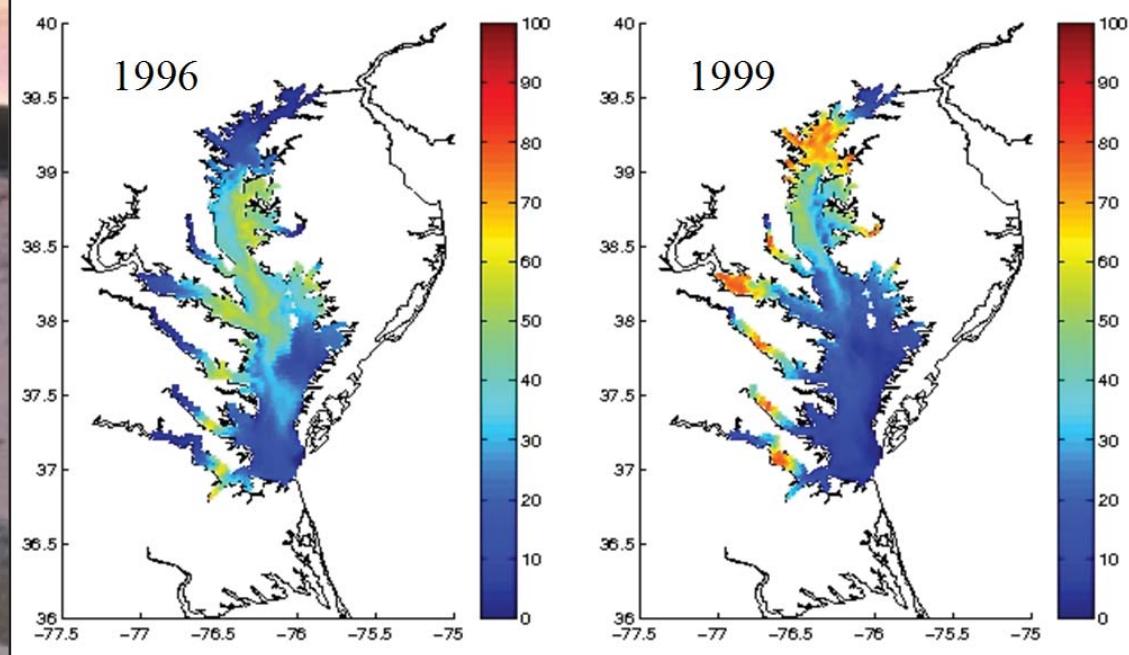
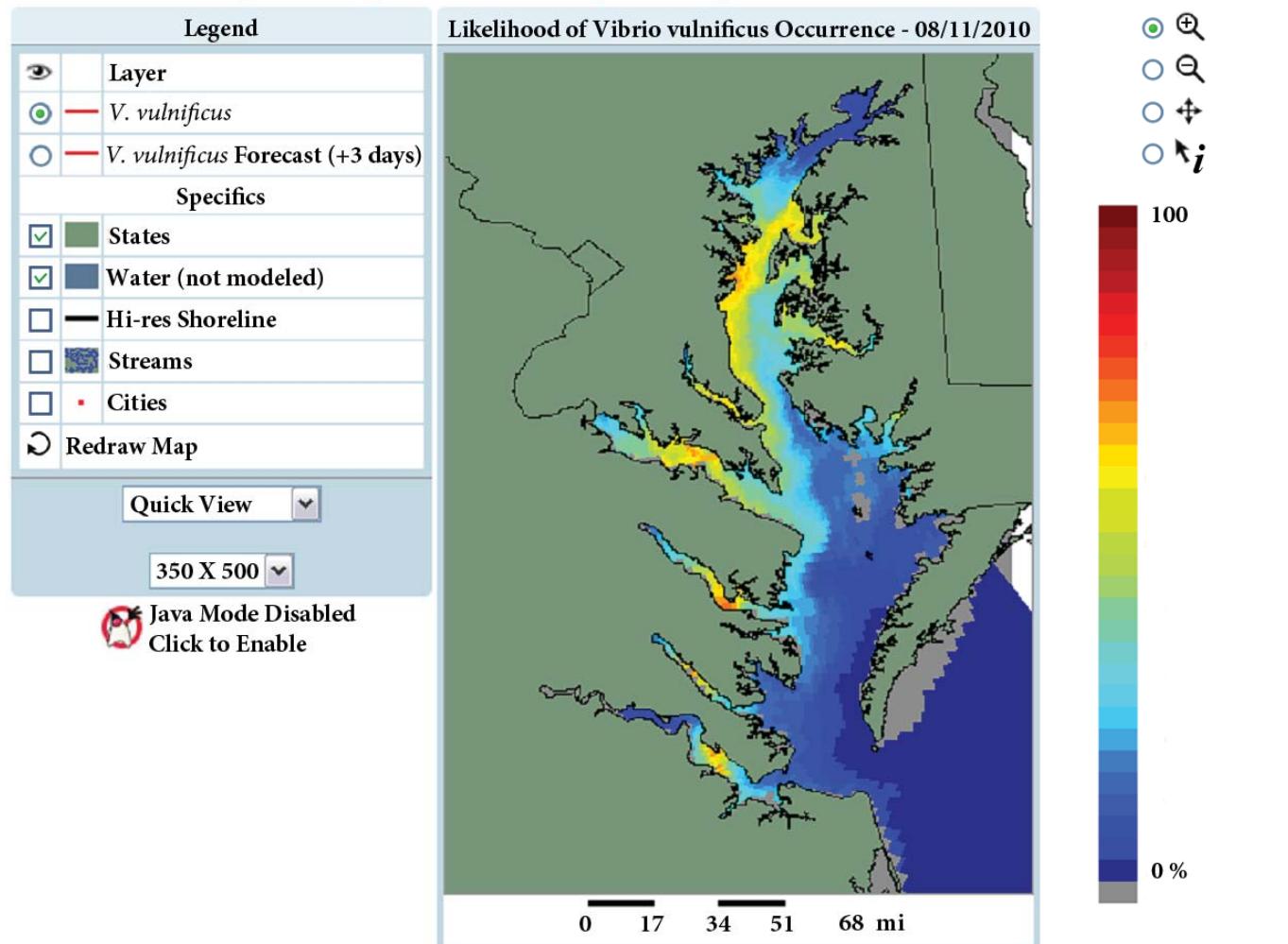


Figure 4. *Vibrio vulnificus* model output for 8/11/2010 and web interface provided to state and county health officials. Scale represents probability of occurrence from 0 (blue) to 100% (red). No data is available for areas shaded gray.

These near-real-time maps of *V. vulnificus* likelihood are experimental products and should be considered provisional.



role in spatial and temporal distribution of the species (Figure 3).

- Current forecasting products are available from a restricted access web platform provided to state and county health officials (Figure 4).
- Additional forecasts for other species of *Vibrio* are being developed.

CONCLUSIONS

The NOAA/NCCOS Pathogen Monitoring and Forecasting Program is conducting the most spatially intensive sampling for potential human pathogens ever attempted in Chesapeake Bay. The efforts are culminating in a suite of models and forecasts being provided to state and county health officials for internal use in management decision making. The *Vibrio vulnificus* model represents the first of these forecasts and clearly demonstrates the strong regulation of distribution by temperature and salinity. Because these variables are modified by climate, large changes in the distribution of *V. vulnificus* can occur annually, and perhaps over longer time frames with potential global climate change.

ACKNOWLEDGEMENTS

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POLLUTION





HABITAT

CHAPTER 12:

Chesapeake Bay Habitat Assessment: Status and Trends of Environmental Conditions for 1985-2006



L. Bahner³, X. Zhang^{2*}, and R. Kelty¹.

National Centers for Coastal Ocean Science¹,

Center for Coastal Environmental Health and Biomolecular Research, Cooperative Oxford Laboratory² - CRC³

*Corresponding author, xinsheng.zhang@noaa.gov, 410-226-5193 (phone), 410-226-5925 (fax)

BACKGROUND

The Chesapeake Bay is a large estuary located in the USA's mid-Atlantic coastal region and is a dynamic, highly productive, and intensively studied ecosystem. The drainage basin stretches across New York, Pennsylvania, Maryland, Delaware, Virginia, West Virginia, and the District of Columbia, spanning approximately 103,000 km². The annual economic benefit from fishing, tourism, property, and shipping activities in the Bay has been valued at up to \$60 billion (Chesapeake Bay Blue Ribbon Finance Panel 2004). Fisheries revenues from the Bay are some of the highest in the nation (Chesapeake Bay Program 2004).

The ecosystem has undergone profound changes since European colonization. Oyster, striped bass, menhaden, and crab, have been heavily exploited (Kemp *et al.* 2005, Williams *et al.* 2010). Twice as many people (almost 17 million) live in the watershed as in 1950 and the population is expected to reach 19 million by 2030 (Boesch and Greer 2003). As forests, farms and other lands are transformed into subdivisions, shopping centers, or parking lots, the hydrology of the Bay watershed is changing. Changes in hydrographic conditions (e.g. temperature, salinity and circulation) are contributing to large-scale alterations in ecosystem structure and function (Pyke *et al.* 2008). This is compounded by climate-driven changes in rain patterns and storm intensity and frequency. A better understanding of the impli-

cations of these changes will help the people who live in, and depend on, the Chesapeake Bay watershed develop effective management and mitigation strategies.

This paper summarizes findings from a metadata analysis in which we track changes in habitat conditions important to fish and shellfish in Chesapeake Bay from 1985 to 2006. These spatially explicit water quality and biological trends provide insight into Chesapeake Bay fish habitat under various hydroclimate scenarios (Figure 1). The trends we detect and document are used as references by the Bay's scientific and management community, and can be used to guide action and measure progress related to the water quality and living resource goals of the 2010 Chesapeake Bay Executive Order.

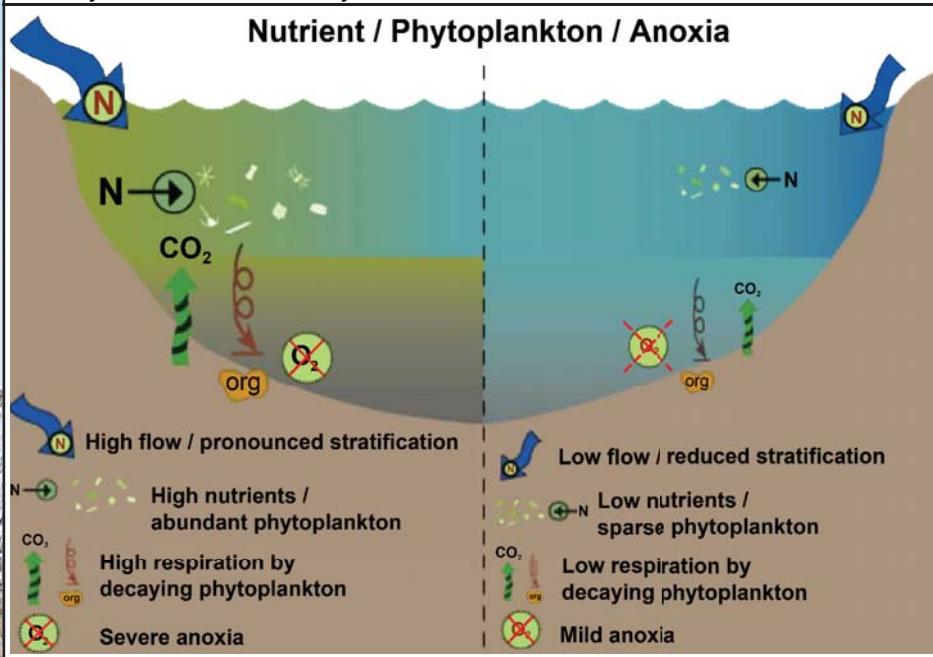
APPROACH

We used the Chesapeake Bay and Tidal Tributary Interpolator to detect trends in water quality and primary and secondary biological state variables (e.g. chlorophyll and zooplankton). These variables are primary determinates of aquatic habitat and food web structure in the Bay. We limited our analysis to the Chesapeake Bay mainstem and tidal tributaries.

Assessment Process

- Water quality and plankton data were obtained

Figure 1. Conceptual diagram of water column structure, nutrient concentrations, phytoplankton abundance and hypoxic/anoxic conditions associated with eutrophication that may result under various hydroclimate scenarios.



from the Chesapeake Bay Program

- Data parameters were aggregated by year, month, station and depth
- Monthly data were spatially interpolated using the Chesapeake Bay and Tidal Tributary Interpolator
- Interpolated data were spatially mapped and analyzed for trends and magnitudes of changes by using linear regression during a 22-year period (1985-2006).

Chesapeake Bay and Tidal Tributary Interpolator

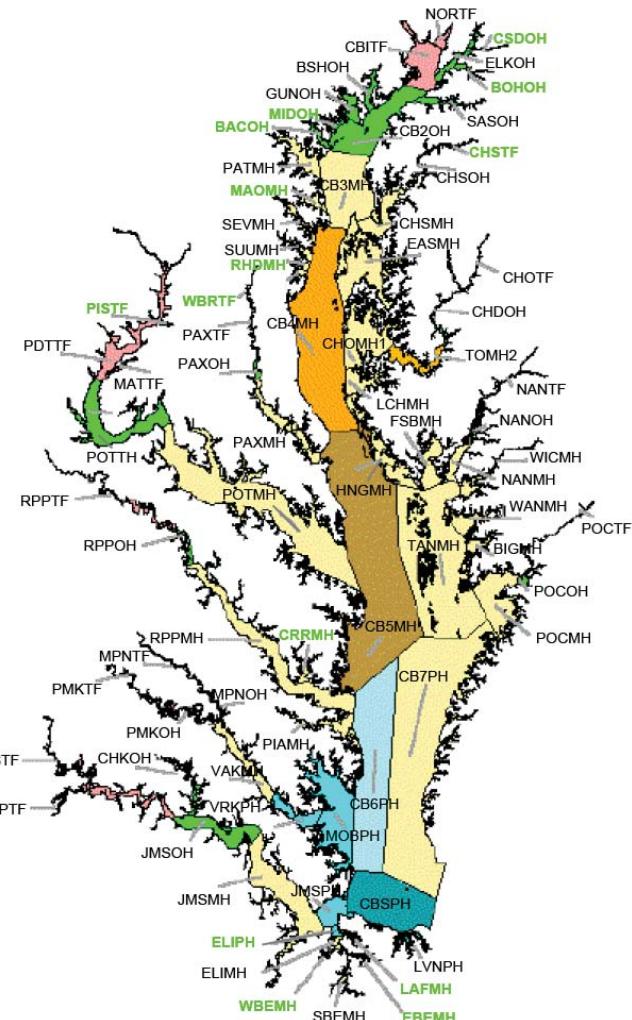
The Chesapeake Bay and Tidal Tributary Interpolator has been used since 1988 to analyze water quality for the Chesapeake Bay Program. The Chesapeake Bay Program adopted a 77-segment segmentation scheme in 1998 that divides the Bay into geographic areas characterized by generally homogeneous environmental conditions (Figure 2). The Interpolator is a cell-based interpolator that computes values for cells from surface to bottom in each of these 77 segments. Cell dimensions have a maximum size in the 8 Main Bay segments (1 km x 1 km x 1m), and are reduced down to the smallest size (50m x 50m x 1m) in several river segments. Tributary rivers are represented by various sized cells depending on tributary geometry, because the narrow upstream portions of rivers require smaller cells to accurately model dimensions of particular riv-

ers. This configuration results in a total of 238,669 depth-specific cells for all 77 segments which comprise the Main Bay and tidal tributaries. Interpolated monitoring data can be mapped to create pictures of data in 2- or 3-dimensions, and can be used to quantify and map trends of water quality parameters as well as fish and shellfish distributions.

KEY FINDINGS

- The interpolator produces easy-to-interpret visual presentations of spatially-articulated Chesapeake Bay Program data from 1985 to 2006. This information can be used to examine water

Figure 2. 1998 Chesapeake Bay Program 77-segment Segmentation Scheme.



quality and biological trends. These output products can also be used to evaluate the impact of, for example, changing demographics and/or land use, and environmental policies and regulation.

- Although not all of the trends reported here are statistically significant, the interpolator based results revealed several trends in key environmental parameters.
- We detected a conspicuous increase in water temperature for Chesapeake Bay on the order of 0.5 to 1.5 degrees C averaged throughout the water column (Figure 3a). In fact, some areas of the Bay have increased up to 2.6 degrees C during the past 22 years with the largest increases evident in the southern portion of the Bay including Tangier Sound (Figure 2 and Figure 3a).
- Salinity during the years 1985 through 1989, at the beginning of the series, was high but declined in more recent years, 2003 through 2006, and overall trends in salinity for Chesapeake Bay and tidal tributaries for the 1985-2006 period are negative with values declining by 1.5 to 2 psu (Figure 2 and Figure 3b).
- Trends in dissolved oxygen (DO) are weak and mixed, with increased DO levels in much of the Virginia portion of the Chesapeake Bay mainstem, and Rappahannock, York, and James Rivers; whereas several Maryland Rivers and the deep trench in the Chesapeake Bay mainstem show declining oxygen over the same 22 year period (Figure 2 and Figure 3c).
- Most areas of the Bay show no long-term trend in total suspended solids during 1985-2006 (Figure 3d). However, total suspended solids decreased in many fresh water segments of Maryland tidal rivers, the upper tidal Potomac River, across the Bay from the Rappahannock River and Tangier Sound, and mid-segments of the York and James Rivers (Figure 2 and Figure 3d). Several areas in Virginia's western shore rivers (Rappahannock, York, and James) indicate an upward trend in total suspended solids that are not assessed fully in this report (Figure 2 and Figure 3d).
- Most of the Bay shows no long-term trend in dis-

solved inorganic nitrogen, laterally or by depth during 1985-2006 (Figure 3e). However, several Western Shore rivers show a long-term downward trend in dissolved inorganic nitrogen, and several Maryland Eastern Shore rivers show a slight upward trend (Figure 2 and Figure 3e).

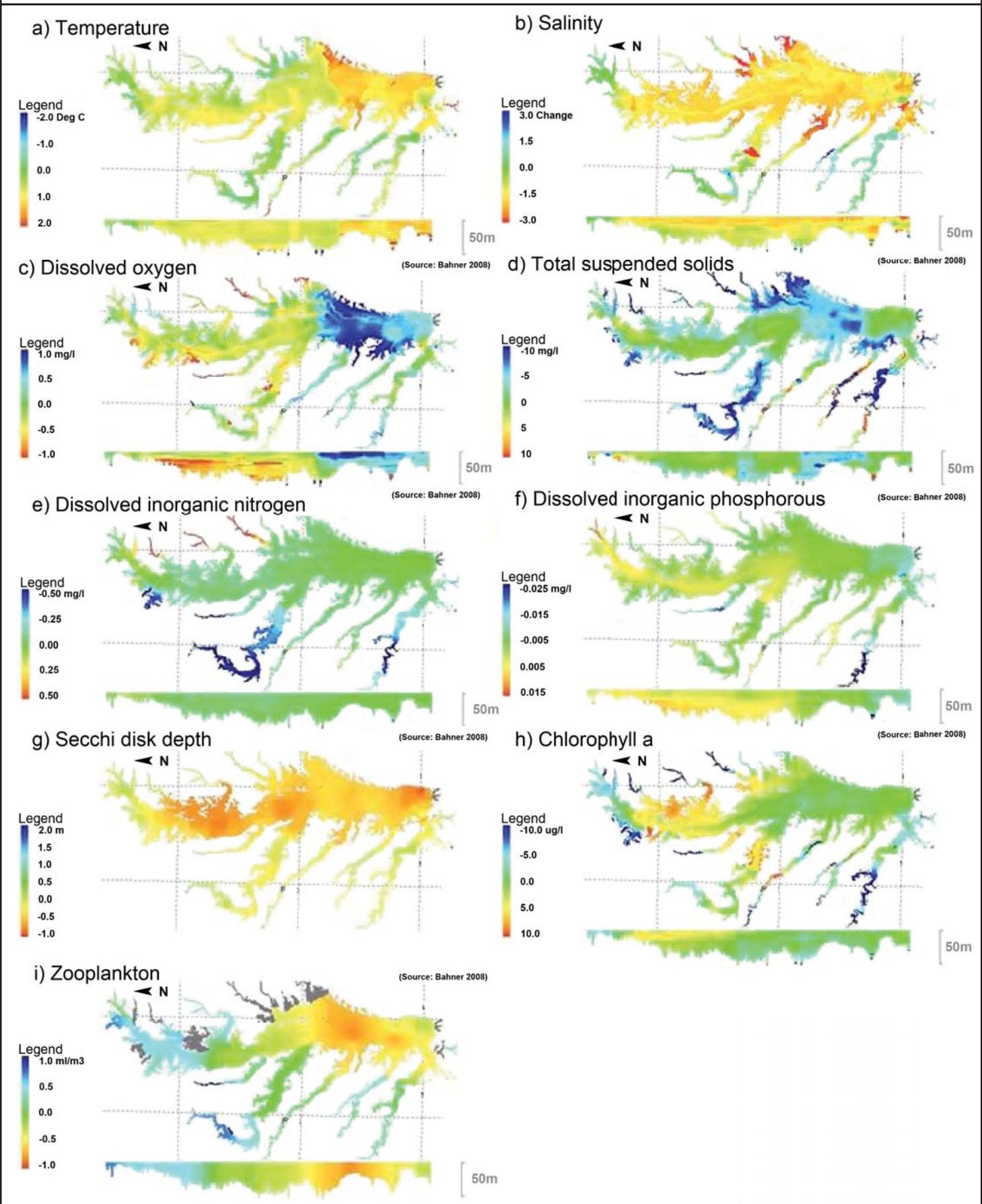
- Slight increases were detected for dissolved inorganic phosphorous in the Maryland portion of the Chesapeake Bay mainstem and lower Potomac River, while several Western Shore rivers show long-term reduction (Figure 2 and Figure 3f). Much of the Virginia portion of the Bay shows a long-term downward trend for phosphorous, laterally and by depth (Figure 2 and Figure 3f).
- Trends in Secchi disk depth are large in magnitude (-0.1m to -0.7m) indicating that water clarity has unexpectedly decreased over most of Chesapeake Bay and lower tributary rivers (Figure 3g). Upper tidal rivers exhibit no trend or a weak positive trend during 1985-2006 (Figure 2 and Figure 3g).
- Trends in chlorophyll-a are mixed with slight increases in the central part of the Maryland portion of the Bay, mid-Patuxent River, and mid-Potomac River (Figure 2 and Figure 3h). Several upper-river areas exhibit reduced chlorophyll-a (Figure 2 and Figure 3h).
- Zooplankton biovolume decreased by approximately 25 to 50% in the Virginia portion of the Bay during 1985 through 2002, while zooplankton biovolume increased by approximately 25% in the Maryland part of the Bay and several tidal tributary rivers (Figure 2 and Figure 3i).

CONCLUSIONS

We present long-term trends and changes in Chesapeake Bay environmental conditions in a spatially explicit format. The physical and biological ecosystem components we examined are essential elements of fish habitat. Data from these individual assessments can be combined using habitat suitability and bioenergetics models to quantify impacts to key fish and shellfish resources (example: Chapter 14 of this report).

The spatially-explicit environmental assessments that we report on here provide information and tools for prioritizing, monitoring, and evaluating effects of different management actions aimed at restoring wa-

Figure 3. Spatially explicit trends and magnitudes of changes estimated by using linear regression in water temperature (a), salinity (b), dissolved oxygen (c), total suspended solids (d), dissolved inorganic nitrogen (e), dissolved inorganic phosphorous (f), Secchi disk depth (g), chlorophyll-a (h) and zooplankton (i) for Chesapeake Bay and tidal tributaries during 1985-2006.



ter quality and habitat at the Bay-wide and tributary scales. They contribute to the scientific basis necessary to develop management approaches and plans that consider the structure and function of the Chesapeake Bay ecosystem (i.e. ecosystem-based management approach). Running a similar analysis in five or ten years will allow us to track and evaluate progress toward water quality and habitat restoration goals in the Bay.

Report from the Chesapeake Bay Program Science and Technical Advisory Committee (STAC), Annapolis, MD. 59 pp.

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CHAPTER 13:

Improving Eelgrass Restoration Site Selection Criteria: Classification of Wave Energy Climate for Eelgrass Seed Establishment



Mark S. Fonseca* and Amit Malhotra.

National Centers for Coastal Ocean Science,
Center for Coastal Fisheries and Habitat Research
Applied Ecology and Restoration Research Branch

*Corresponding author, mark.fonseca@noaa.gov, 252-728-8729 (phone), 252-838-0809 (fax)

INTRODUCTION

Coastal managers and ecologists are often confronted with situations where a quantitative knowledge of wave parameters would significantly improve their ability to interpret shoreline stability issues, ecosystem function, habitat distribution and restoration potential. Here, as part of a larger research project being conducted at the Virginia Institute of Marine Science funded by the Army Corps of Engineers we are working to improve eelgrass restoration site selection criteria by quantifying the hydrodynamic conditions under which eelgrass seedling establishment can be achieved.

Extensive work has been done on forecasting water circulation, especially that driven by astronomical tides and tidal stage and current speed forecasts are readily available online for many coastal systems. In contrast, wave energy forecast tools are few (e.g., SWAN¹, GLERL², HISWA³), are frequently intimidating to the uninitiated and in general do not appear as an independent variable in many integrative studies. Also, equipment for measuring waves tend to be more expensive and complex because sampling requires a carefully considered temporal component that must have high sampling frequency to characterize a wave, but must also be able to assess episodic, comparatively unpredictable (versus tides) events. As a result, the quantita-

tive consideration of wind wave effects in shallow water environments has not yet become a regular part of the ecologists' or coastal managers' tool box.

Wind waves can profoundly impact the environment in coastal areas. To forecast their effects, however, involves estimating the wave energy reaching a given point by taking into account the effects of wind, local topography and bathymetry. We will utilize NOAA's Wave Exposure Model (WEMo)⁴ that considers the effect of the aforementioned physical parameters to produce quantitative associations of locally-generated wind wave energy in association with the eelgrass restoration effort. More recently, this model has been modified to produce predictions of benthic shear stress:

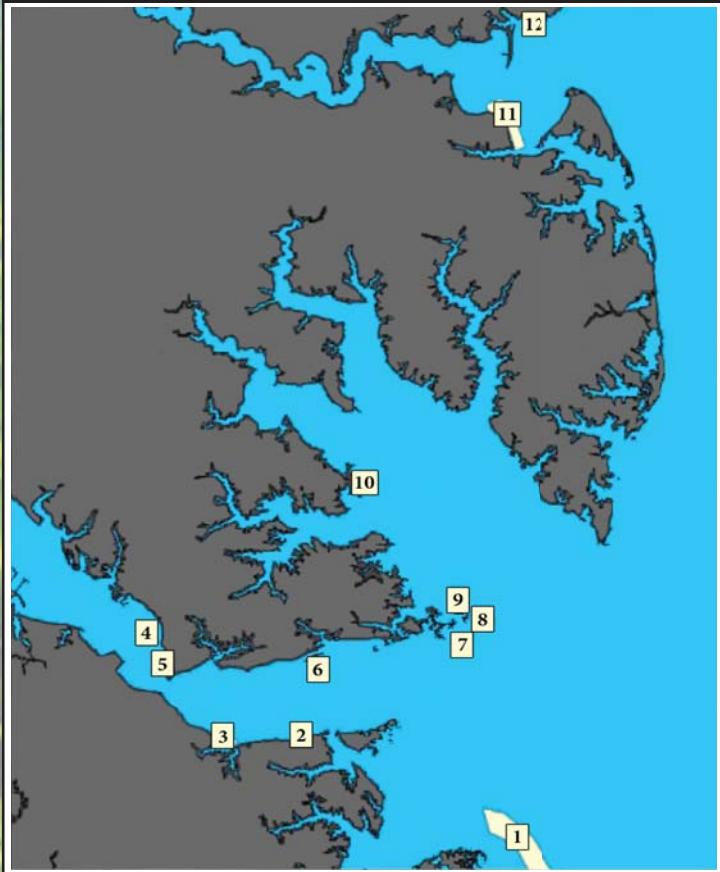
$$\tau_w = \mu (\partial u / \partial y) \Big|_{y=0}$$

Where τ_w = shear stress, μ = viscosity and $\partial u / \partial y$ = change in velocity with depth above the sediment surface; and horizontal shear velocity:

$$u^* = \sqrt{\tau_w / \rho}$$

Where u^* = shear velocity and ρ = fluid density; which together can be used to estimate a Shields' parameter function predicting the initiation of motion for

Figure 1. Potential eelgrass seedling planting sites.



sediment at these restoration sites (Fisher *et al.* 1983). In this project we will ultimately use WEMo to hindcast wave and benthic shear conditions during times when eelgrass (*Zostera marina L.*) seeds were lost in past projects and use those findings to predict suitably protected areas for testing seed deployments. More immediately, we needed to test the new benthic shear stress module and simultaneously rank proposed eelgrass seeding sites for potential limitation by wave energy.

METHODS

We downloaded wind data from the Piney Point wind station (PPTM2: 38.133N 76.533W) and used WEMo to compute representative wave energy at a dozen potential seedling restoration sites (Fig. 1). We also conducted a comparison of predicted versus observed orbital velocities in the York River ($37^{\circ}14' 54''$ N, $76^{\circ} 30' 25''$ W) near the Virginia Institute of Marine Sciences campus in Gloucester Point, Virginia. An acoustic Doppler current meter (Nortek Vector Velocimeter; high resolution 3D),

was deployed to collect the velocity data ~5cm above the sea floor. The current meter was set to record velocity data in east, north and up (ENU) coordinate system in 4.25 minute bursts with a sampling rate of 8 Hz every 30 minutes from 8 January 2010 to 11 January 2010. In order to compare these field data with the predicted (WEMo) orbital velocity, the east and north components of vector data were extracted corresponding to the horizontal orbital velocities calculated by WEMo. The sensor data were further filtered by only taking the average of the top 2% of the absolute value of orbital velocities for every burst to avoid the canceling effect of averaging the otherwise sinusoidal orbital velocities.

Wind data for York River site was obtained from the York River East Rear Range Light station (National Data Buoy Center station YKRV2). The wind data obtained were in hourly increments with wind speed (ms^{-1}) and wind direction (degrees from true north) for the period of deployment of the sensors. Wind data were compiled using 2 hours of data with steps of 1 hour creating 67 wind files. A 6 hour moving average analysis was done on observed and calculated velocity data as this has been shown to be the most parsimonious time

Figure 2. Representative wave energy (Joules m^{-1} wave crest) for the 12 sites shown in Figure 1.

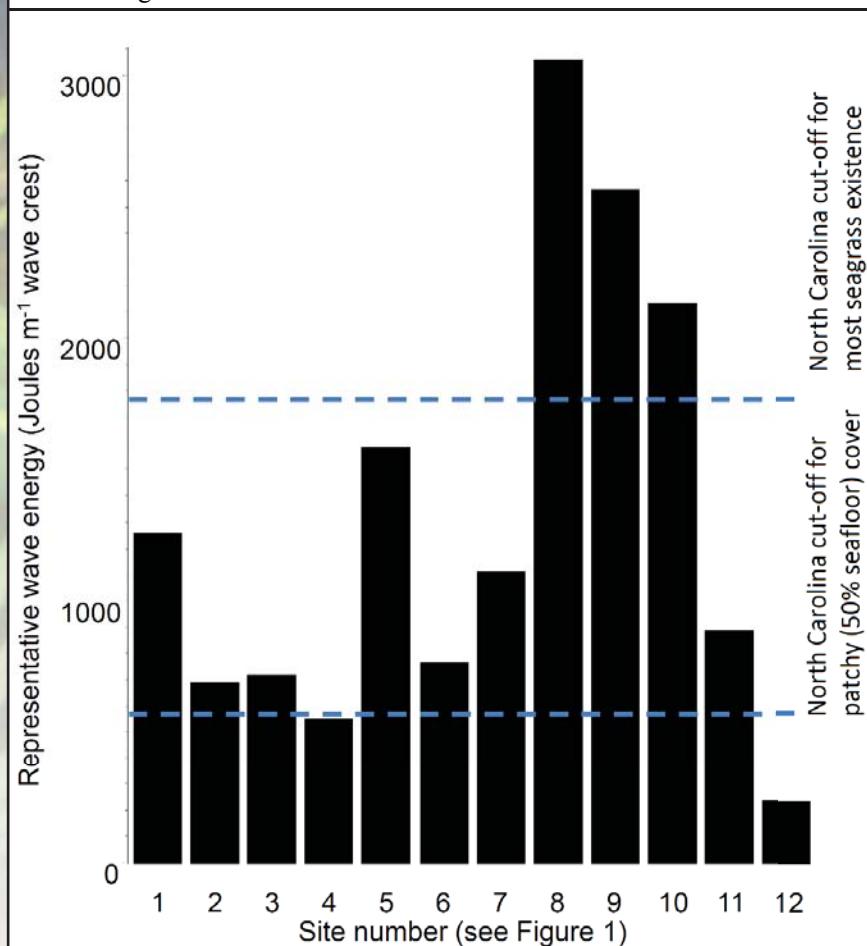
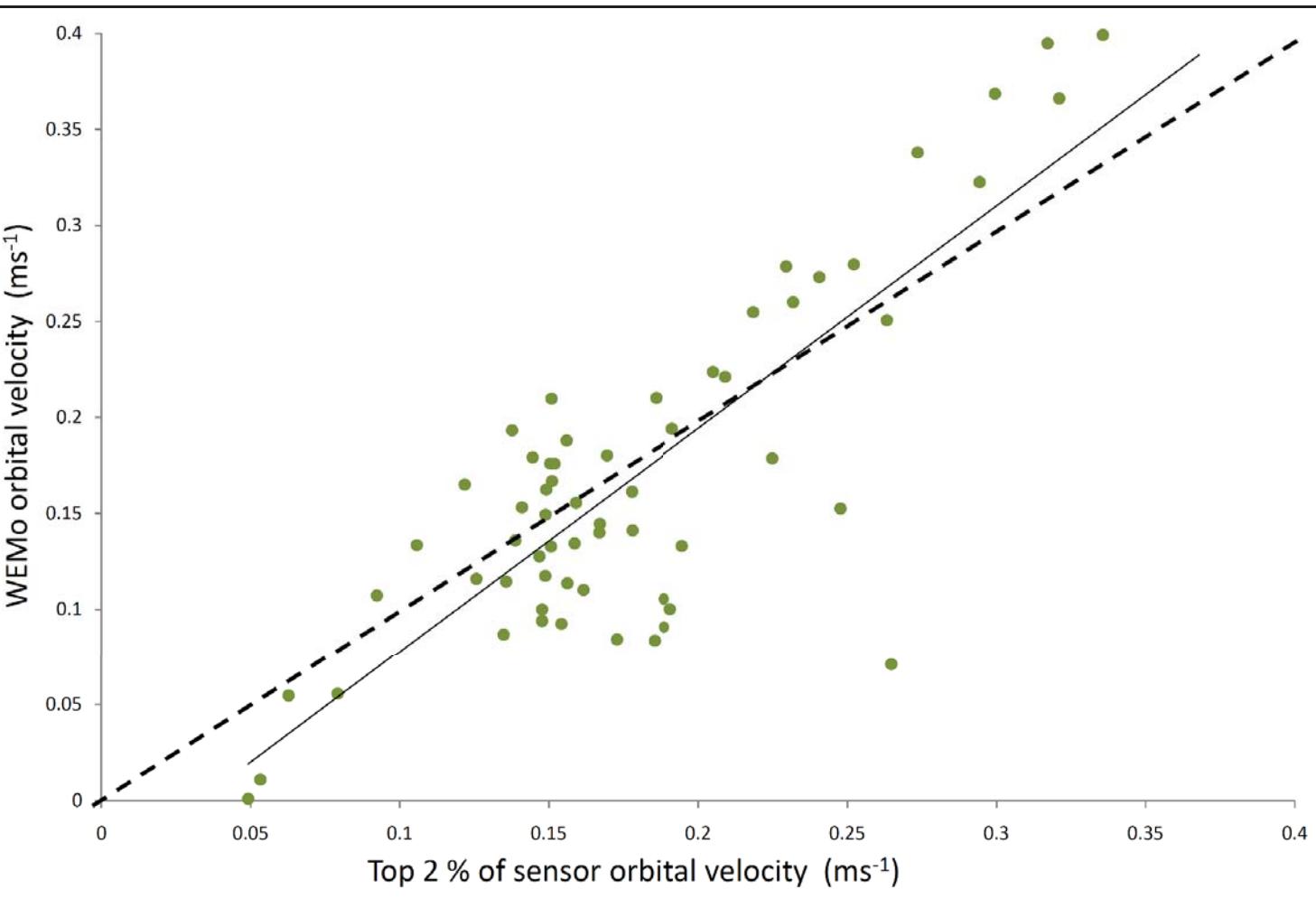


Figure 3. Virginia, York River predicted (by WEMo) near-bed orbital velocity versus observed from sensor. Solid line = best fit linear regression; dashed line = 1:1 correspondence.



frame for obtaining useful temporal coherence under WEMo (Malhotra and Fonseca, *in review*, *Limnology and Oceanography: Methods*).

RESULTS

The (representative) wave energy assessment of the various potential test sites indicated that many sites exceeded the wave energy threshold for the same species of seagrass as seen elsewhere (Fig. 2; comparison with North Carolina seagrass based on recalculation of Fonseca and Bell's 1998 study sites using wave energy as opposed to their preliminary calculations using a dimensionless index).

The field trial comparing predicted versus observed orbital velocity values indicated strong coherence of (Fig. 3) and a pattern of response that was similar to the generally acceptable PR and SI values for significant wave height (performance rate: 0.52 [unity = perfect model], Scatter index: 0.54 [values approaching 0 = perfect conformance]) in that these values are very similar to the values obtained for wave energy modeling

results for currently accepted models like SWAN and HISWA.

DISCUSSION

The addition of a benthic shear stress module as tested here appears to extend the utility of the model as a user-friendly software. The model utilizes easily available input data and has relatively low computer processing and memory requirements that can rapidly return accurate hindcasts and forecasts of key wind wave metrics. From these preliminary trials, it appears that the model can predict benthic shear accurately but many locations under consideration for eelgrass restoration may experience wave energy too high for persistent eelgrass colonization.

ENDNOTES

¹ <http://vlm089.citg.tudelft.nl/swan/index.htm> (July 25, 2008)

² GLERL; Schwab, D. J., J. R. Bennett, P. C. Liu, and M. A. Donelan (1984), Application of a simple numerical wave prediction model to Lake Erie, *J. Geophys. Res.*, 89, 3586– 3589.

³ HISWA

⁴ <http://www.csc.noaa.gov/digitalcoast/tools/wemo/index.html>

⁵ Seed Burial as a Site Selection Tool for Enhancing Initial Eelgrass; Orth *et al.* 2009.

CHAPTER 14:

Chesapeake Bay Striped Bass Habitat Suitability and Bioenergetics Modeling and Forecasting: From Physics to Fish



X. Zhang^{1*}, L. Bahner², R.J. Wood¹, E.J. Martino¹, S.A. Ludsin³, R. Murtugudde⁴, M.B.K. Prasad⁴, R.R. Hood⁵, and W. Long⁵.

National Centers for Coastal Ocean Science,

Center for Coastal Environmental Health and Biomolecular Research, Cooperative Oxford Laboratory¹ - CRC²

The Ohio State University, Department of Evolution, Ecology, and Organismal Biology³

University of Maryland, Earth System Science Interdisciplinary Center⁴

University of Maryland Center for Environmental Science, Horn Point Laboratory⁵

*Corresponding author, xinsheng.zhang@noaa.gov, 410-226-5193 (phone), 410-226-5925 (fax)

BACKGROUND

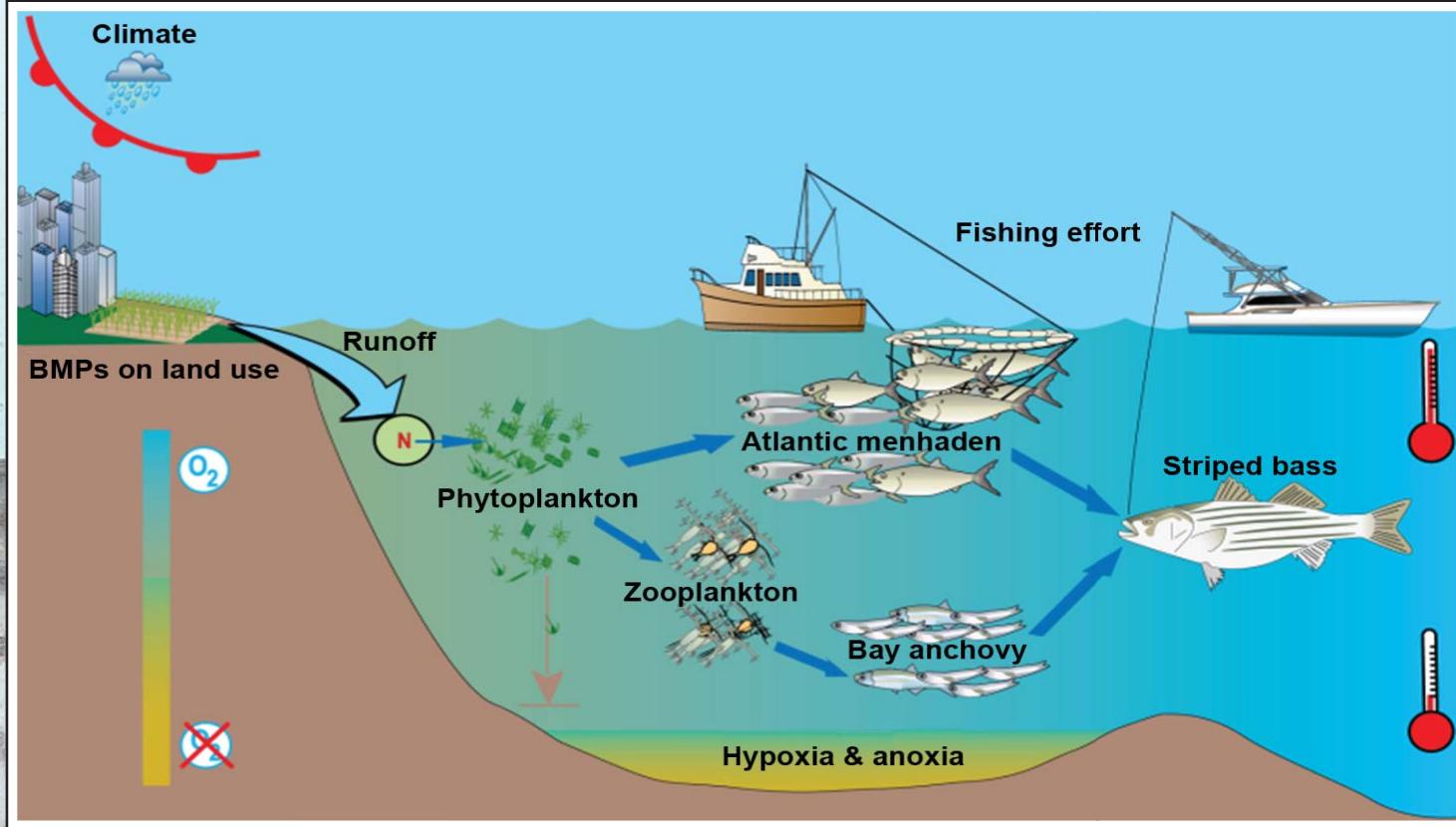
Striped bass (*Morone saxatilis*) support important commercial and recreational fisheries in Chesapeake Bay (Figure 1). The striped bass population in Chesapeake Bay dropped to historically low levels in the early 1980s and was declared recovered in the middle 1990s. Managers have been working to develop and implement scientifically- and economically-based management policies to maintain a healthy striped bass population that supports a sustainable fishery (FEP 2006). However, our knowledge of effects of habitat conditions on striped bass population dynamics is very limited. Therefore, defining habitat preferences for striped bass and understanding and forecasting potential effects of differences in habitat quality and quantity on striped bass distribution and physiology are important from both scientific and resource management perspectives. Chesapeake Bay has experienced severe hypoxia since the 1950s (Hagy *et al.* 2004; Kemp *et al.* 2005). Bottom hypoxia in Chesapeake Bay can occur from spring to fall, and typically peaks during summer when severe hypoxia can occupy almost all sub-pycnocline waters in the central mesohaline section of the Chesapeake Bay (Hagy *et al.* 2004; Zhang *et al.* 2006). This large volume

of hypoxic water may subsequently reduce the quantity and quality of suitable habitat for striped bass. This report investigates and forecasts the status and trends in Chesapeake Bay striped bass habitat based on habitat suitability and bioenergetics models during a 22-year period (1985-2006). The geographic range of this assessment is the Chesapeake Bay mainstem and tidal tributaries to the Bay. The findings in this report can be used to guide to management decisions on meeting water quality and living resource goals established by the 2010 Chesapeake Bay Executive Order (i.e. Goals of Restore Clean Water, Recover Habitat, and Sustain Fish and Wildlife).

APPROACH

Our objective was to develop a suite of striped bass habitat suitability and bioenergetics models that can be used to evaluate and forecast how hydro-climate variability drives variability in habitat quality and quantity. To do this, we combined habitat suitability and bioenergetics models to the "Chesapeake Bay and Tidal Tributary Interpolator" software to produce easy-to-interpret maps that spatially-articulate Chesapeake Bay striped bass habitat quality and quantity. Particular em-

Figure 1. Conceptual diagram illustrating selected key ecological and economic components and their connections.



phasis was placed on summer conditions, when Coutant (1985) hypothesized that a temperature-oxygen “squeeze” could affect striped bass in Chesapeake Bay through effects on predator-prey habitat overlap/separation and predator-prey encounter rates (Figure 2).

Habitat suitability models

The Habitat Suitability Index (HSI) modeling approach published by Bain and Bain (1982) was adapted to calculate an index (HSI) scaled from 0 (unsuitable habitat conditions) to 1 (optimal habitat conditions) for any organism, such as striped bass, or group of organisms using defined habitat requirements. We evaluated

only effects of the two dominant environmental parameters, water temperature and dissolved oxygen on striped bass. The individual HSI scores are combined in one of three ways: 1) minimum – the minimum of the individual HSI scores is selected as the combined score; 2) geometric mean – the geometric mean of the individual HSI scores is calculated by multiplying the HSI scores and then the nth root of the resulting product is taken as the combined score; and in this report we define a third method for estimating synergistic effects, 3) multiplicative – the individual HSI scores are multiplied together to calculate the combined score. The HSI is a valuable tool for evaluating habitat conditions over

Figure 2. Conceptual diagram illustrating effects of temperature-oxygen “squeeze” on striped bass and prey habitat overlap/separation and encounter rates.

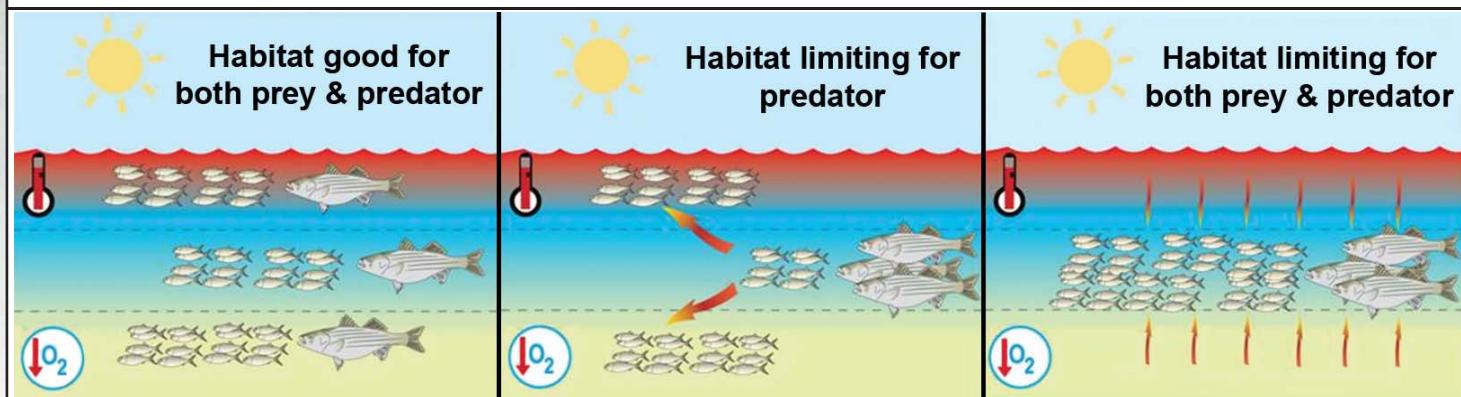
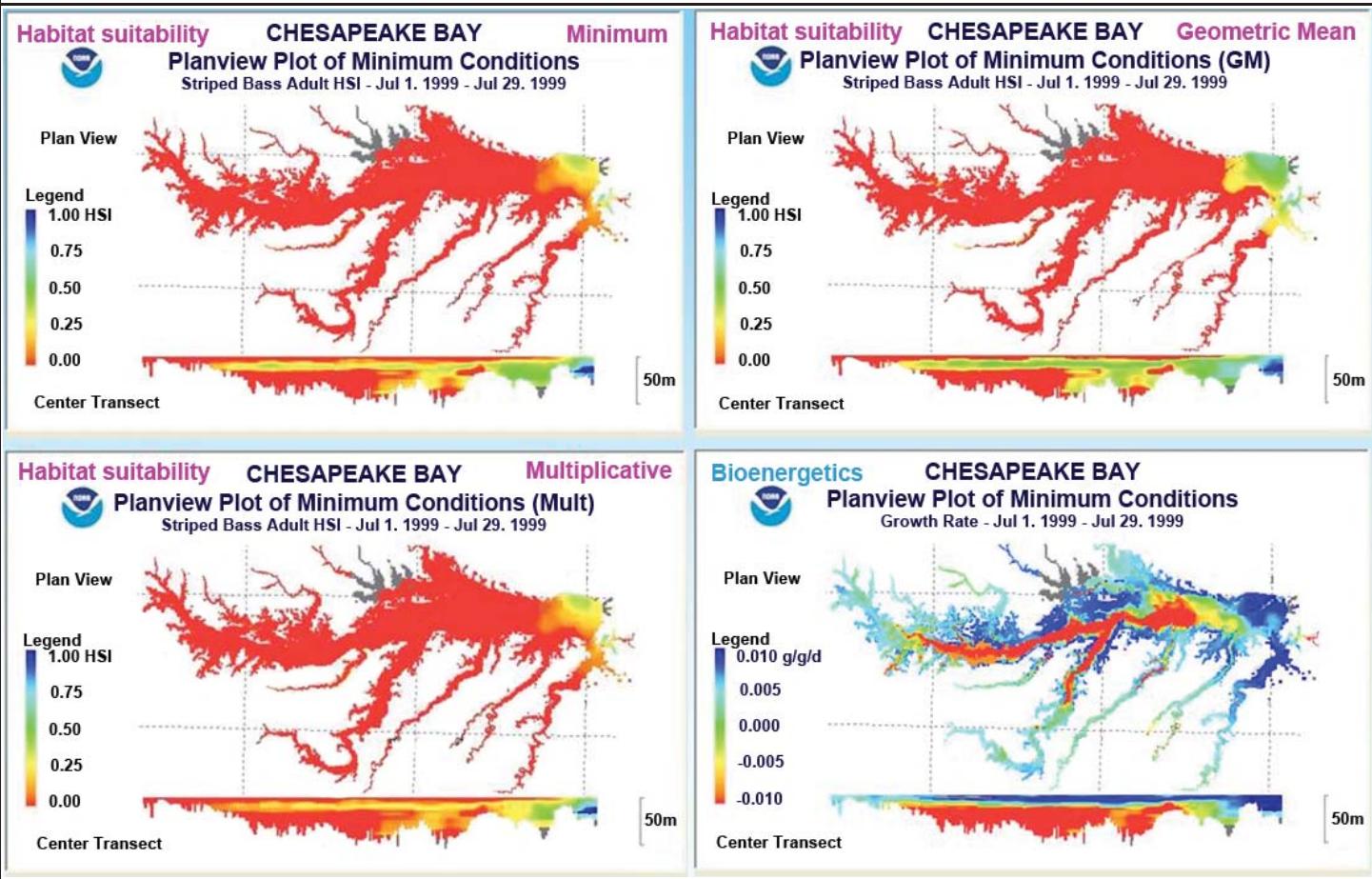


Figure 3. Estimated habitat suitability index and growth rate potential based on habitat suitability and bioenergetics modeling in July 1999.



space and time, and these techniques can be applied for other species and in other geographic areas. HSI can also be used as a management prioritization tool, by calculating HSI models for different species, then determining which parameters have the most influence on a suite of organisms, and using that information to prioritize resources for restoration and conservation programs.

Bioenergetics models

Fish have certain basic requirements: oxygen to breathe, food to eat, and sheltered locations to avoid predators, rest, and reproduce. Fish growth rate potential (GRP) can be estimated with bioenergetics models. These models use a mass-balance approach to trace the energy in consumed food through the pathways of growth, respiration, and export of waste. Fish growth rate potential has been used as a measurement of fish habitat suitability (Brandt and Kirsch 1993; Hartman and Brandt 1995; Costantini *et al.* 2008; Ludsin *et al.* 2009). In our spatially-explicit model of fish growth rate, space is modeled as an explicit attribute of the environment by subdividing the water column into a se-

ries of rows and columns that define a grid. Each cell in the grid is characterized by a specific hydrographic condition and prey density. A foraging model converts the prey densities in each cell to a fish consumption level. A species-specific bioenergetics model then calculates a potential growth rate from the predicted consumption. The model outputs a growth rate potential, or the

Figure 4. Seasonal variability of estimated striped bass habitat suitability index and growth rate potential based on habitat suitability and bioenergetics modeling for the years 1985-2006.

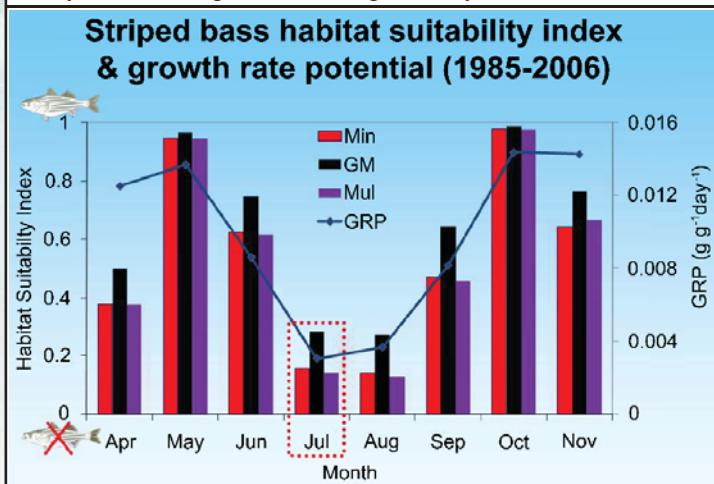
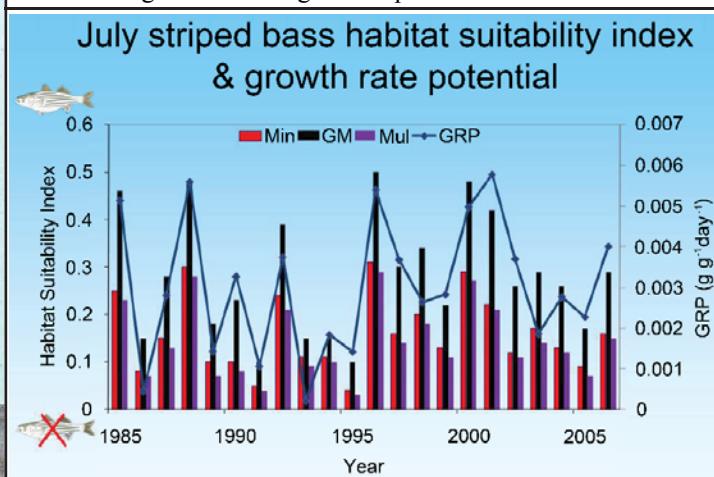


Figure 5. Inter-annual variability of estimated striped bass habitat suitability and growth rate potential based on habitat suitability and bioenergetics modeling for the period of 1985-2006.



growth rate a fish might achieve if placed in a given cell given the specific habitat quality of that cell. The model assumes that within each cell, prey items are randomly distributed (Brandt *et al.* 1992). Growth rate models can be refined to closely model growth as functions of habitat conditions and to provide quantitative estimates of growth which is not possible with simpler habitat suitability models. Growth rate models can be further enhanced to estimate population productivity of a species given additional assumptions.

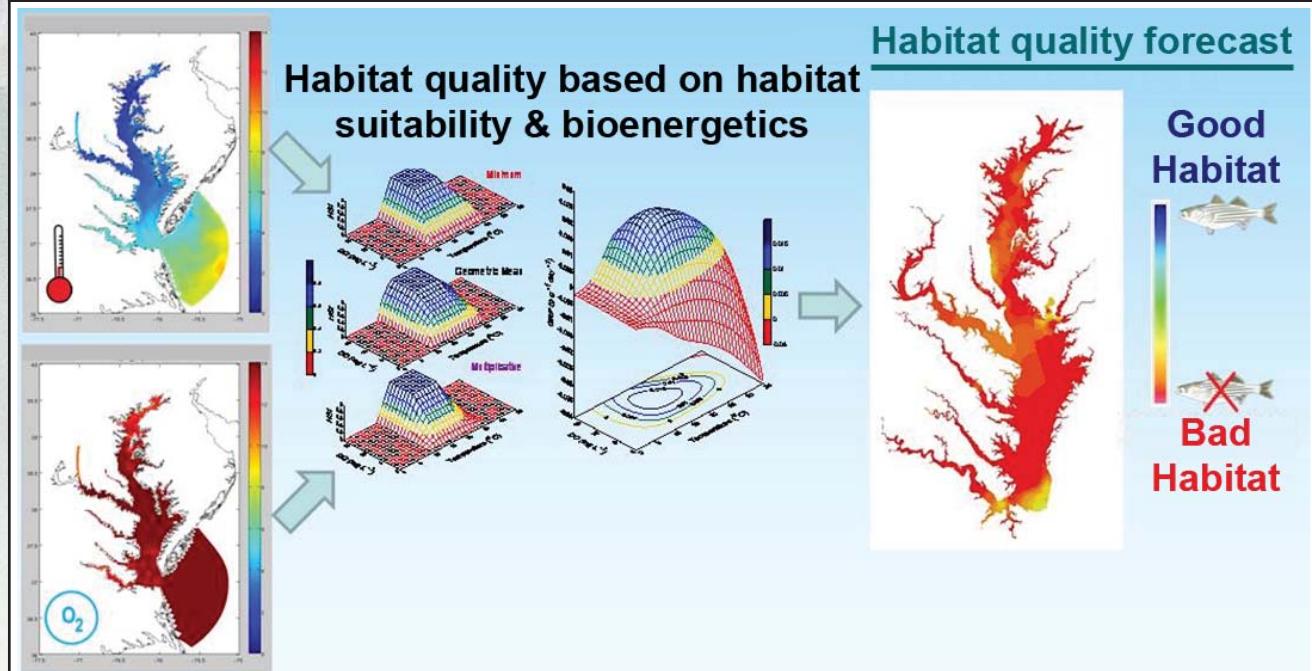
This report provides a brief comparison of growth rate and HSI models. HSI models provide a means to examine habitat suitability based on assumptions of how habitat conditions affect various organisms.

Growth rate models can be refined to closely model organism growth as a function of habitat conditions and to provide quantitative estimates of growth which are not calculated by HSI models. In this report, both HSI and GRP models are implemented in a spatial context and by month over a 22 year period providing one approach for linking habitat conditions to fish quantities and distributions by space and time.

KEY FINDINGS

- Results of both habitat suitability and bioenergetics models suggest that high summer surface temperature and low dissolved oxygen might squeeze striped bass to the more suitable habitat in the middle layer of the water column (Figure 3). However, more research and observation are needed to further refine and ground-truth these suggestive relationships between temporal and spatial variability in habitat quality and striped bass distribution (i.e. where the fish are).
- Habitat suitability index scores based on the geometric mean of individual scores tend to produce a higher score than those based on the minimum and multiplicative combination of individual scores (Figure 4, see APPROACH section for technical details). Habitat suitability index scores based on the minimum and multiplicative methods are very similar. The growth rate potential (GRP) estimated

Figure 6. Integrate striped bass habitat suitability and bioenergetics models into the Chesapeake Bay Ecological Forecasting System.



from a bioenergetics model follows a trend that is similar to that based on a habitat suitability index (Figure 4). Lowest habitat conditions are found in July and August, when water temperatures and dissolved oxygen push the limits of striped bass tolerance (Figure 4).

- Results of both habitat suitability and bioenergetics models suggest strong inter-annual variability in striped bass habitat conditions (Figure 5). Although the mechanisms driven the annual variability are still not well understood, the extensity of hypoxic conditions associated with eutrophication and climate change/variability might be the key driver.

CONCLUSIONS

Our findings suggest that habitat conditions do indeed affect striped bass biology and ecology. The temperature-oxygen “squeeze” could affect striped bass in Chesapeake Bay through effects on production, carrying capacity, predator-prey habitat overlap/separation and encounter rates, and vulnerability to pathogens. Time series of habitat suitability and growth rate potential estimates could be used as input into other models, such as the Chesapeake Bay Fishery Ecosystem Model (Christensen *et al.* 2009), to determine to what extent variations in habitat condition are associated with fish population dynamics. Relationships between habitat conditions and population dynamics will vary depending on the sensitivity of particular species to habitat conditions. Alternatively, the connection between habitat condition and fish population dynamics may be less important for species that are most heavily impacted by predation or fishing pressure. The striped bass habitat suitability and bioenergetics models are part of the Chesapeake Bay Ecological Forecasting Modeling System that links atmospheric, hydrodynamic, water quality, and living resource sub-models to produce operational and accessible models relevant to Bay restoration efforts (Figure 6). One ultimate objective is to provide managers with decision-support tools with forecasting capacities for integrating climate, land use, and ecosystem structure and function for ecosystem-based fisheries management (i.e. from physics to fish).

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CHAPTER 15:

Modeling Atlantic Menhaden Recruitment in the Chesapeake Bay: Is the Striped Bass Recovery a Problem?



X. Zhang^{*1}, R.J. Wood¹, E.J. Martino¹, E.D. Houde², H. Townsend³, and C. Wicks⁴.

National Centers for Coastal Ocean Science,

Center for Coastal Environmental Health and Biomolecular Research, Cooperative Oxford Laboratory¹

UMCES, Chesapeake Biological Laboratory²

NOAA, NMFS, HC, NCBO, Cooperative Oxford Laboratory³

EcoCheck (NOAA-UMCES partnership), NCBO, Cooperative Oxford Laboratory⁴

*Corresponding author, xinsheng.zhang@noaa.gov, 410-226-5193 (phone), 410-226-5925 (fax)

BACKGROUND

Fisheries management is gradually moving from a single-species approach toward a multi-species and ecosystem-based approach. Ecosystem-based fisheries management requires consideration of not only targeted fish species, but also the influences of social, physical, and biological interactions that affect the targeted fishery. Atlantic menhaden (*Brevoortia tyrannus*) play an important role in Chesapeake Bay as a direct trophic link between primary production and striped bass (*Morone saxatilis*) and other sport and commercial fishes. Menhaden are a major component of older striped bass diets (Hartman and Brandt 1995; Walter and Austin 2003). Atlantic-coast menhaden spawning stock is reasonably healthy, but localized overfishing has been a concern recently (Figure 1). In contrast, menhaden recruitment in Chesapeake Bay is 5 – 10 times lower now than in the 1980s (Figure 1). Although specific mechanisms responsible for the recent decline in menhaden recruitment are

not known, the recent decline in recruitment is likely determined by the combined effects of increased predation from fish such as striped bass, climate variability, and plankton prey availability (Figure 2). Predation can be a potent regulator of recruitment (Hunter 1984; Walters *et al.* 1986) and its interaction with growth rate may be the regulatory mechanism of recruitment through

Figure 1. Menhaden spawning stock biomass along the Atlantic coast of North America, menhaden recruitment in the Maryland portion of Chesapeake Bay, and striped bass (age2+) biomass along the Atlantic coast of North America.

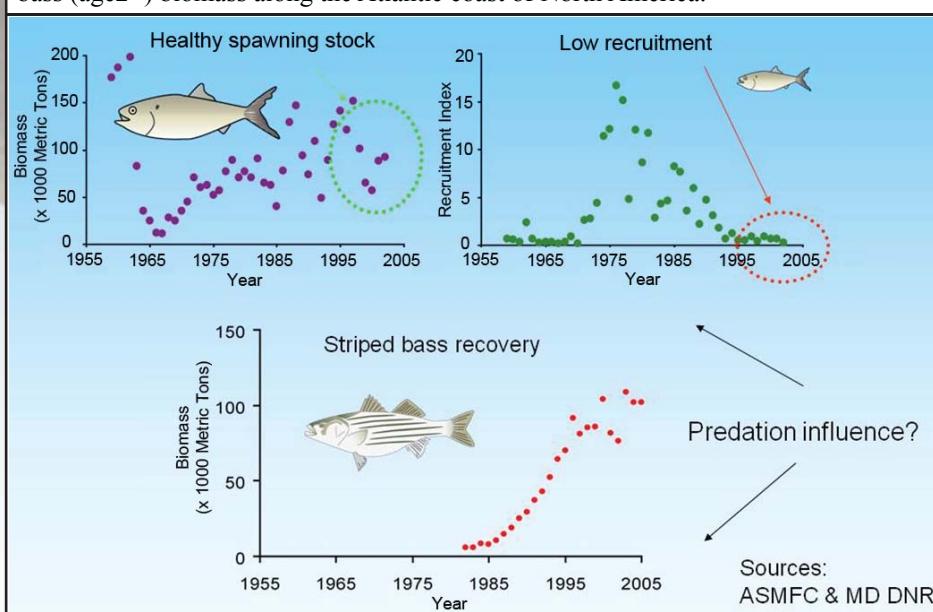
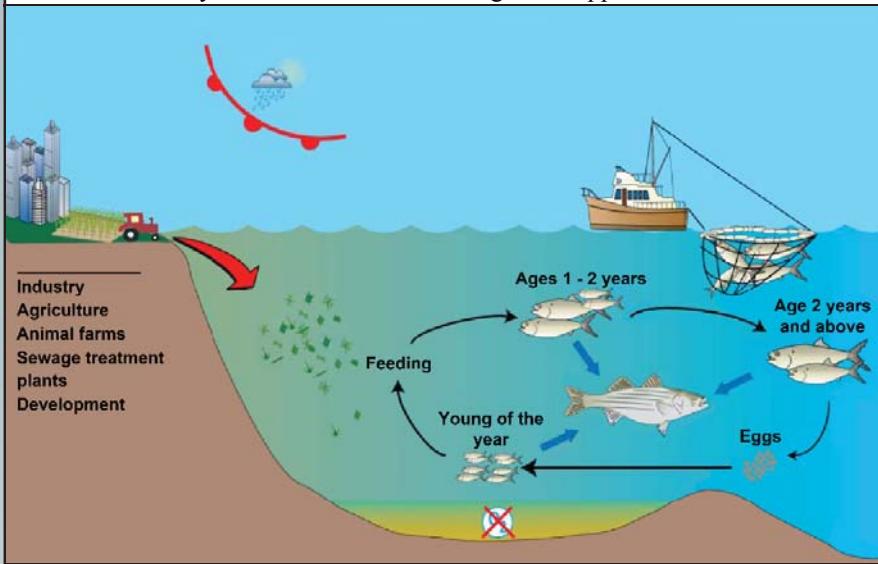


Figure 2. Conceptual diagram illustrating some of the key elements comprising a menhaden ecosystem based fisheries management approach.



size-selective mortality. This work used a modeling approach to test the often-referenced role of striped bass predation on Chesapeake Bay Atlantic menhaden recruitment.

APPROACH

Chesapeake Bay menhaden recruitment data was acquired from the Maryland Department of Natural Resources (MD DNR), Fisheries Service juvenile striped bass seine survey (<http://www.dnr.state.md.us/fisheries/juvindex/index.html>). There is no data available for "Chesapeake Bay" menhaden spawning stock biomass thus we used Atlantic coast-wide menhaden spawning stock biomass as an index for spawners that contribute to Chesapeake Bay recruitment. Atlantic coast-wide menhaden spawning stock biomass was acquired from the ASMFC Atlantic menhaden stock assessment (ASMFC 2004). Atlantic coast-wide striped bass biomass was acquired from the ASMFC stock assessment (ASMFC 2005), and we used age-2+ striped bass biomass as an index of potential striped bass predation on age-0 menhaden in Chesapeake Bay. Striped bass commercial landings for Chesapeake Bay were extracted from the NOAA Fisheries Statistics and Economics Division online database (<http://www.st.nmfs.gov>).

Stock-recruitment analysis normally consists of looking at the

empirical relationship between the spawning stock size, and the subsequent recruitment of the year class produced by that level of spawners. According to standard Ricker stock-recruitment theory (1954), the stock-recruitment relationship can be represented with equation 1:

$$R = \alpha S e^{-\beta S}$$

Equation 1

where R is the recruitment, S is the level of spawning stock biomass, α is the recruits-per-spawner at low spawner biomass and represents density-independent mortality due to intraspecific competition or cannibalism, and β describes how quickly the recruits-per-spawner drop as S increases and represents additional density-dependent mortality due to intraspecific competition or cannibalism.

In this study, we extended the standard Ricker stock-recruitment model (Equation 1) to account for potential effect of striped bass predation on menhaden recruitment (Equation 2).

$$R = \alpha S e^{-(\beta S - \gamma P)}$$

Equation 2

where P is the biomass of striped bass predators. The parameter γ should be negative and is interpreted as the fraction of prey stock consumed per predator prior to prey recruitment.

To test the accuracy of the extended menhaden stock-recruitment Ricker model including striped bass

Figure 3. Estimates of striped bass biomass from 1958 to 1981. Estimates based on a significant relationship ($r^2=0.92$) between striped bass biomass and landing during the 1982 to 2002 period.

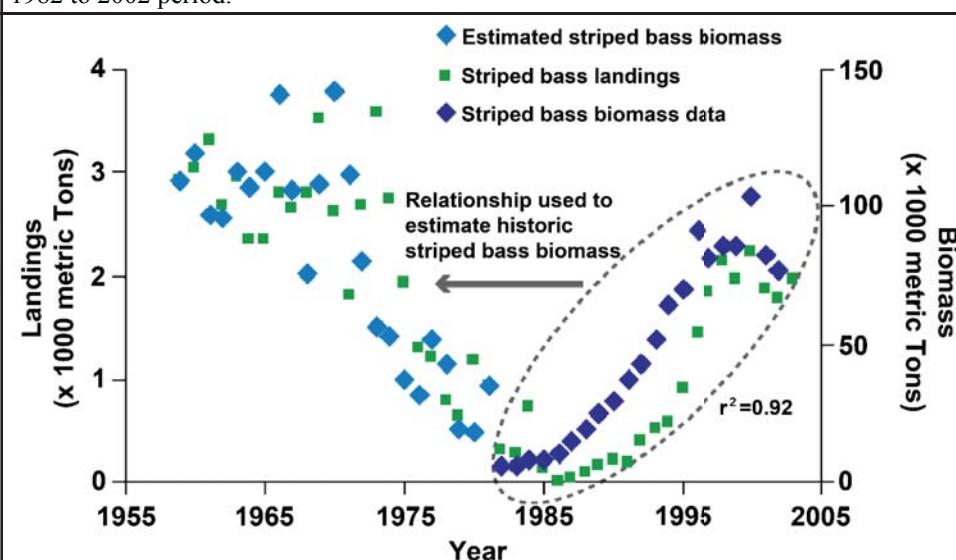
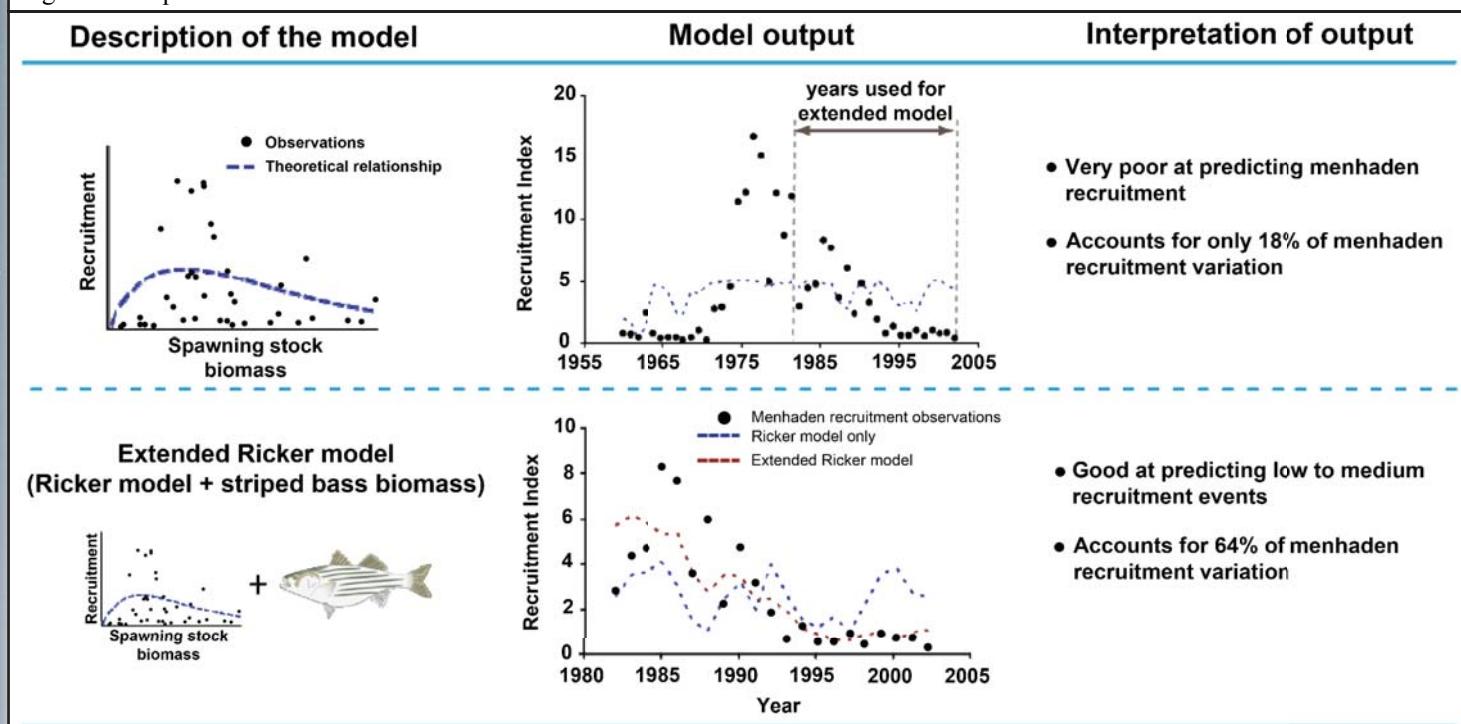


Figure 4. Outputs based on the standard and extended menhaden stock-recruitment Ricker models.



predation, we used a hindcasting technique to assess model accuracy on historical data not included in the model development. The extended Ricker model was constructed using data after 1982. Hindcasting measured how well the model simulates recruitment from 1958-1981. Hindcasting required an estimation of historic striped bass biomass because all available biomass data (1982-2002) was used in developing the model. Estimation of striped bass, for the purpose of hindcasting only, was based on: (a) a strong ($r^2=0.92$) empirical relationship between coast-wide age-2+ striped bass biomass and 3-year lagged Chesapeake striped bass commercial landings for the 1982-2002; and (b) historic Chesapeake Bay striped bass landing data (1958-1981) (Figure 3).

KEY FINDINGS

- The standard Ricker stock-recruitment model provided a poor fit to the relationship between spawner biomass and menhaden recruitment, and is only minimally useful as a management tool (Figure 4).
- The menhaden stock-recruitment Ricker model incorporating striped bass biomass was a much better predictor of menhaden recruitment, and provided a reasonably good

prediction for low and medium recruitment events (Figure 4).

- Thus, extended stock-recruitment Ricker models that incorporate several environmental parameters, and their interactions, can be helpful for moving toward ecosystem-based fisheries management.
- However, despite the statistical association between striped bass biomass and menhaden recruitment, the established predator-prey relationships and significant association detected may not be a result of

Figure 5. Hindcast of menhaden recruitment in Chesapeake Bay based on the extended menhaden stock-recruitment Ricker model modified to include striped bass predation and observed recruitment data.

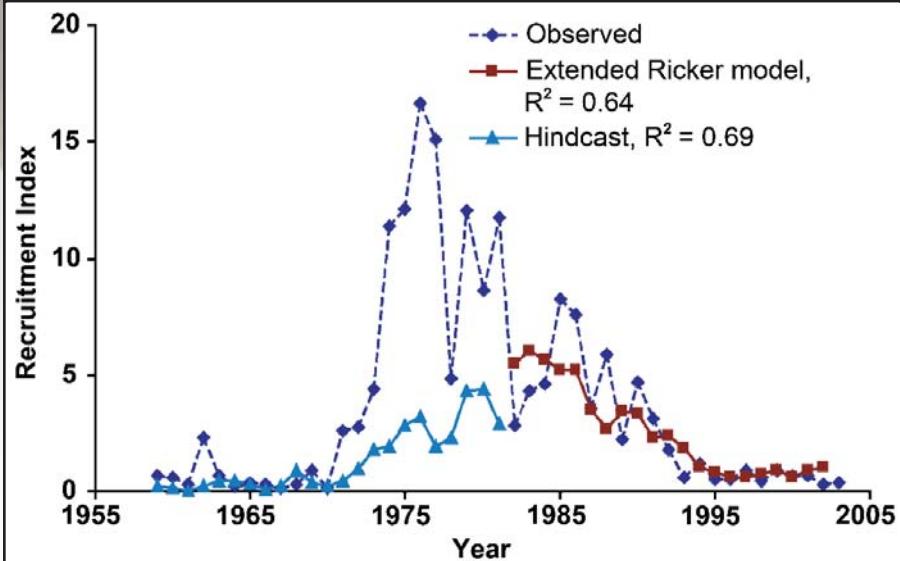
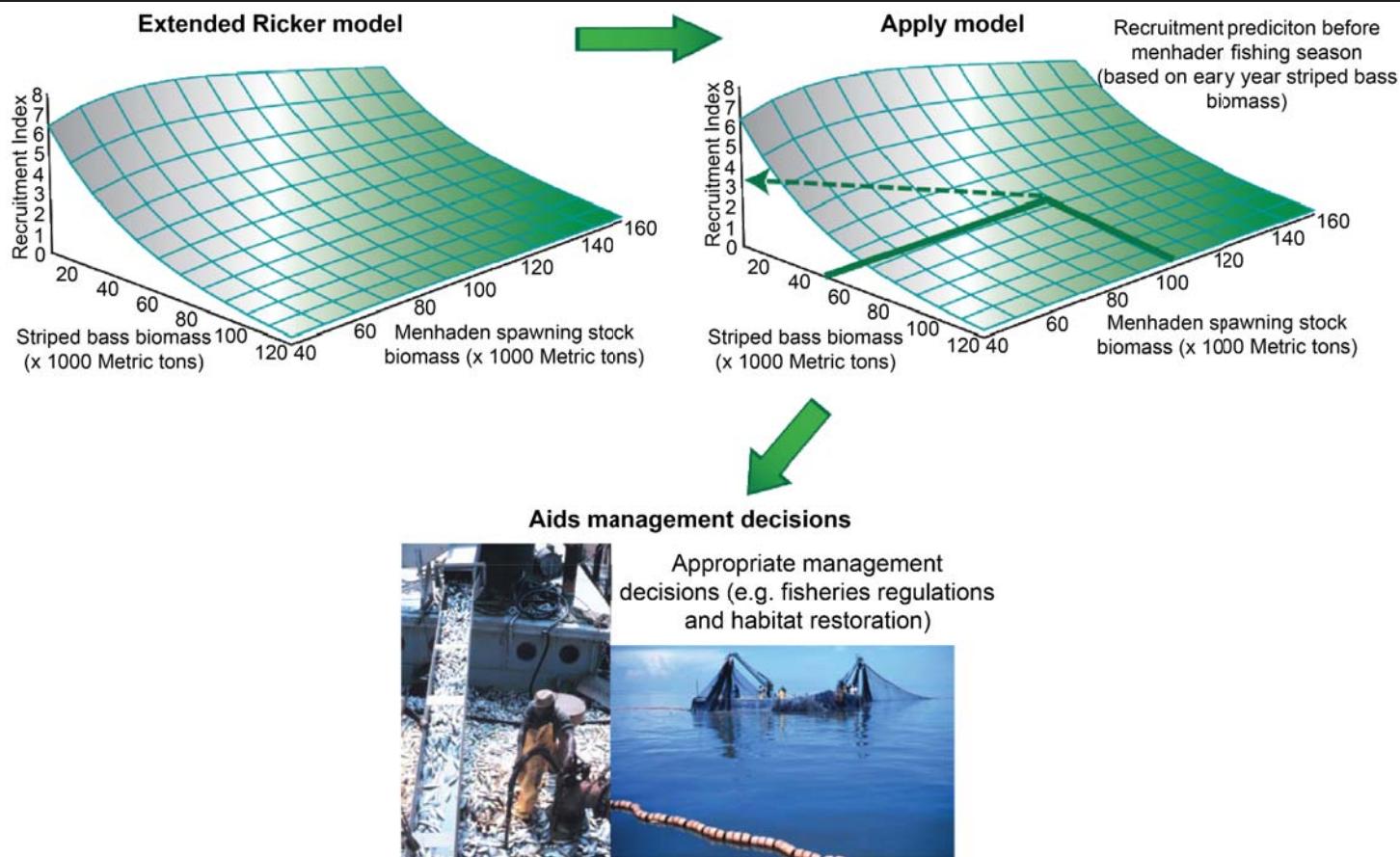


Figure 6. Incorporation of model into menhaden fisheries management.



cause and effect relationships.

- The extended menhaden stock-recruitment Ricker model including striped bass predation exhibited reasonably good hindcast accuracy when compared to historic menhaden recruitment data (Figure 5).
- Accuracy of the extended Ricker model hindcast was optimum in low recruitment years (1960s) and poor in high recruitment years (1970s), and the overall accuracy was generally good ($r^2=0.69$, Figure 5). Poor model accuracy during high recruitment years highlights the need for further research and model refinement before this model can be used as a management tool. Our ongoing research includes assessing the potential non-linearity of recruitment data, and the inclusion of hydroclimate variability effects.

CONCLUSIONS

The extended menhaden stock-recruitment Ricker model including striped bass predation accounts for both the number of menhaden spawners and the potential effects of striped bass predation, and provides a foundation for developing a more comprehensive

management tool to support management of Chesapeake Bay menhaden. The model could inform managers when the menhaden stock deviates from expected patterns, and provide explanations for the deviations. In addition, this modeling strategy can be used as a prototype that can be adapted for other exploited fish species. Therefore, results from this research could greatly assist in the development of a broader ecosystem-based fisheries management approach in Chesapeake Bay (Figure 6).

ACKNOWLEDGEMENTS

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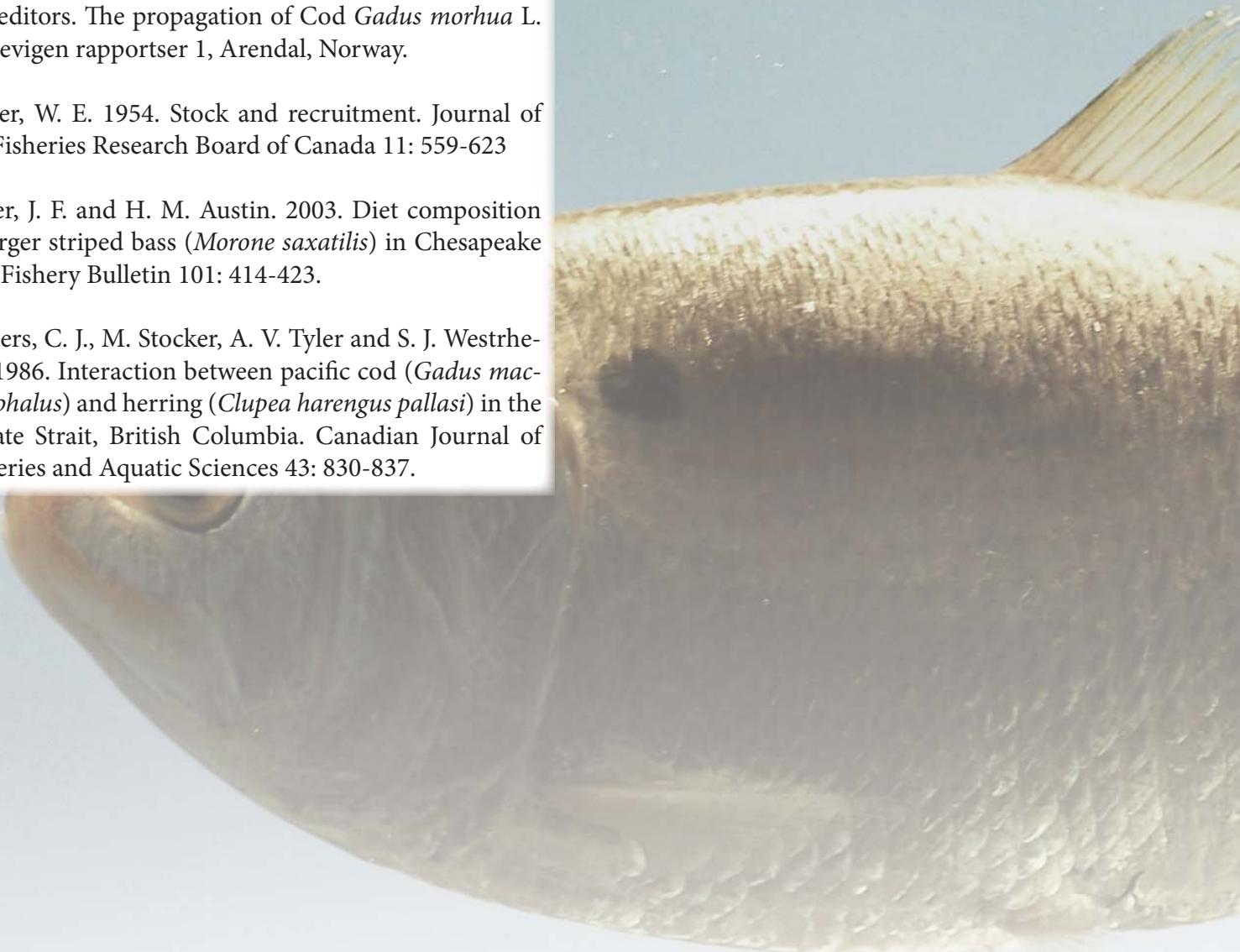
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HABITAT

CHAPTER 16:

The Effects of Dissolved Oxygen on Recreational Striped Bass Catch in the Chesapeake Bay



Andrew L. Mason*
National Centers for Coastal Ocean Science,
Center for Coastal Monitoring and Assessment

*Corresponding author, andrew.mason@noaa.gov, 301-713-3028, x227 (phone), 301-713-4384 (fax)

BACKGROUND

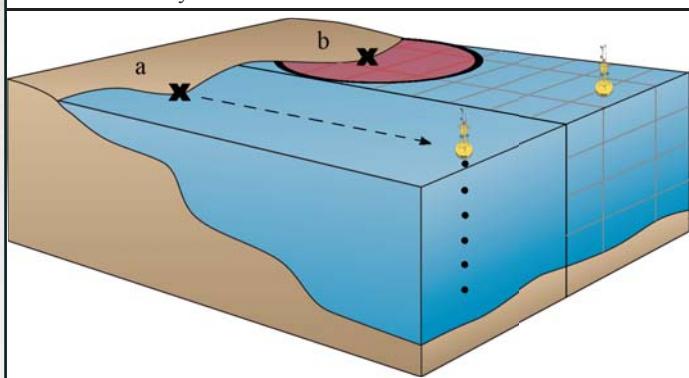
Degraded dissolved oxygen (DO) conditions in the coastal US including the Chesapeake Bay have been increasing since the early 20th century (Boesch and Brinsfield 2000; Diaz and Rosenberg 1995). Hypoxic and anoxic trends in the Chesapeake Bay over this time period have expanded from the deeper mid and lower channel regions up into the upper Bay and some of the major tributaries, including the Patuxent and Potomac rivers (CBP 2008; Kuo and Neilson 1987; Officer *et al.* 1984; Simon 1984; Taft *et al.* 1980; Tuttle *et al.* 1987). This pervasive low DO problem, which stems from anthropogenic sources of nutrients, has wide ranging impacts for the marine environment including loss of habitat (Boesch *et al.* 2001), changes in growth and feeding in marine organisms (Dauer *et al.* 1992; Van der Oost *et al.* 2003), and changes in marine diversity (Dauer *et al.* 1992).

Low DO and other secondary results of nutrient inputs and eutrophic conditions in turn significantly affect human uses of coastal waterbodies, including negative impacts to recreational fishing (Bricker *et al.* 2006; Massey *et. al.* 2006), human health (Anderson *et al.* 2000), and boating (Lipton and Hicks 1999; Lipton and Hicks 2003). For recreational fishing, low DO causes changes in fish distribution (Bricker *et al.* 2006) and feeding habits (Van der Oost *et al.* 2003) which impact where, when, and if fishermen catch fish.

Traditionally, the study of water quality degradation focuses on how human activities affect coastal water quality. However, there has recently been increased interest in the inverse relationship: how water quality affects human uses of coastal waters and estuaries (US EPA 2005). Researchers have tried to quantify, analyze, and predict the effect of water quality on human uses of coastal waters through the use of indicators (Bricker *et al.* 2006; Lipton and Hicks 1999; Lipton and Hicks 2003; Massey *et al.* 2006). These human-use indicators serve to describe a portion of the overall effect that degraded water quality have on human uses of coastal waters.

The extent of the impact of low DO on recreational fishermen in US estuaries was explored by Bricker *et al.* (2006) through the use of a model that links changes in DO to changes in fish catch based on

Figure 1. Examples of point sampling data (a) and interpolated data (b) used for this study.



point water quality measurements. An alternate method is the use of interpolated water quality data, which describes more accurately the water quality in a given area (Figure 1). Mason (2008) adapted the work of Bricker *et al.* (2006) for the Chesapeake Bay and the Patuxent and Potomac rivers using interpolated data. Using one-way analysis of variance (ANOVA), contingency table analysis, and logistic nominal regression the statistical significance of DO's relationship on recreational fish catch of striped bass (*Morone saxatilis*) in the Chesapeake Bay was analyzed.

APPROACH

Data for striped bass catch were obtained from the National Marine Fisheries Service (NMFS) Office of Science and Technology's (OST) Marine Recreational Inventory Initiative (MRII). The MRII program has been collecting data since 1979 in all coastal states except Texas, Hawaii, Alaska, and U.S. territories (Gray *et al.* 1994).

Water quality data used for this analysis came in two parts. Salinity, temperature, and DO point data for the 2000-2006 time period came from the EPA's Chesapeake Bay Program's (CBP) online data hub (CBP 2008), while interpolated DO data, representing 13,000 one meter² surface cells and variable additional one meter² cells depending on depth at a particular location, were received by direct request (Linker pers. comm. 2007). Interpolated data are calculated by using monitoring data from over 50 stations throughout the Bay and its tributaries. The water quality data at these stations, including water quality measurements down the water column, are combined (with a minimum of four measured values) at fixed distances of one kilometer or less in order to produce a three-dimensional average value for the one meter square cell. The two water quality datasets were merged by date and then parsed out by

depth.

Water quality data was merged with Striped bass catch and fisherman data using both SAS and JMP statistical analysis software. The two datasets were merged by location and date with the final dataset being comprised of a unique identification code representing one fisherman's total Striped bass catch on a particular date. Each region was subset from this total merged dataset for the entire Chesapeake Bay.

Following Lipton and Hicks (2003) and Bricker *et. al.* (2006), the expected recreational fish catch was modeled as a function of environmental variables and fisherman-related variables.

$$C_{f,r} = \alpha + \beta_1 MC_r + \beta_2 HRSF_{f,r} + \beta_3 FDAY_f + \beta_4 BSALIN_r + \beta_5 BTEMP_r + \beta_6 BDO_r + \beta_7 (BDO_r)^2 + \beta_8 (BDO_r * BTEMP_r)$$

(Where $C_{f,r}$ is the estimated catch of recreational fisherman f , in area r , representing the sub-regions of the Chesapeake and the Chesapeake as a whole. MC_r is the mean catch of all fishermen fishing in region r . $HRSF$ represents the number of hours spent fishing during the interviewee's recreational fishing trip. $FDAY$ captures the fisherman's skill by showing how many days in the past year the fisherman was out fishing. The environmental variables are characterized by $BSALIN$, $BTEMP$, and BDO representing bottom water salinity, bottom water temperature, and bottom water DO respectively. In addition to these environmental variables, BDO was included as a squared term. This is because in quadratic form, the squared term is expected to have a negative coefficient and as such the effect of increased DO on fish catch would decrease with increasing DO concentrations. BDO was also crossed with $BTEMP$ to further explore habitat interaction effects on fish catch.)

Table 1. Modelled parameter estimates and their significance at the 95th percentile for each region of study in the Chesapeake Bay.

	Model R-Square	Mean Catch (β_1)	Hours Fished (β_2)	Days Fished in Previous 12 Months (β_3)	Bottom Salinity (β_4)	Bottom Temperature (β_5)	Bottom Dissolved Oxygen (β_6)	Bottom DO ² (β_7)	Bottom DO x Bottom Temperature (β_8)
	MC	HRSF	FDAY	BSALIN	BTEMP	BDO	BDO ²	BDO * BTEMP	
Chesapeake Bay	0.0459	0.3674	0.1379	-0.0001	-0.0042	0.0743	0.8995	-0.0355	-0.0073
Upper Bay	0.1444	0.3747	0.1167	0.0008	-0.0688	0.1736	0.7676	-0.0776	-0.0135
Middle Bay	0.0856	0.3603	0.1201	-0.0004	-0.1038	-0.1482	0.6797	-0.0679	0.0209
Lower Bay	0.0443	0.4564	0.1607	0.0001	-0.0192	-0.0181	-0.0027	-0.0005	0.0011
Patuxent River	0.1825	0.6589	0.2084	0.0005	-0.0509	0.0250	-0.9799	0.0800	0.0050
Potomac River	0.1716	0.2527	0.3442	0.0138	-0.4222	-0.8600	0.3616	0.1680	0.1360

= significant at the 95th percentile

= not significant at the 95th percentile

Table 2. Summary of non-parametric DO cluster and frequency analysis.

	No Catch Included		No Catch Excluded		
	Cluster Analysis	Frequency Analysis	Cluster Analysis	Frequency Analysis	
Chesapeake Bay	All	EX	NS	EX	NS
	25th	UC	UC	UC	IR
	10th	EX	IR	UC	NS
Upper Bay	All	UC	NS	UC	NS
Middle Bay	All	EX*	NS	NS	NS
	25th	UC	EX	EX	NS
	10th	EX	EX	EX	EX
Lower Bay	All	EX*	NS	NS	NS

*Denotes where expected results deviated only in that the high DO (>12 mg/L) corresponded to no catch (NC).

IR = Inverse expected relationship shown in both extreme categories. Represents approximately 10%.

EX = Generally expected outcome. Represents approximately 55% of significant results.

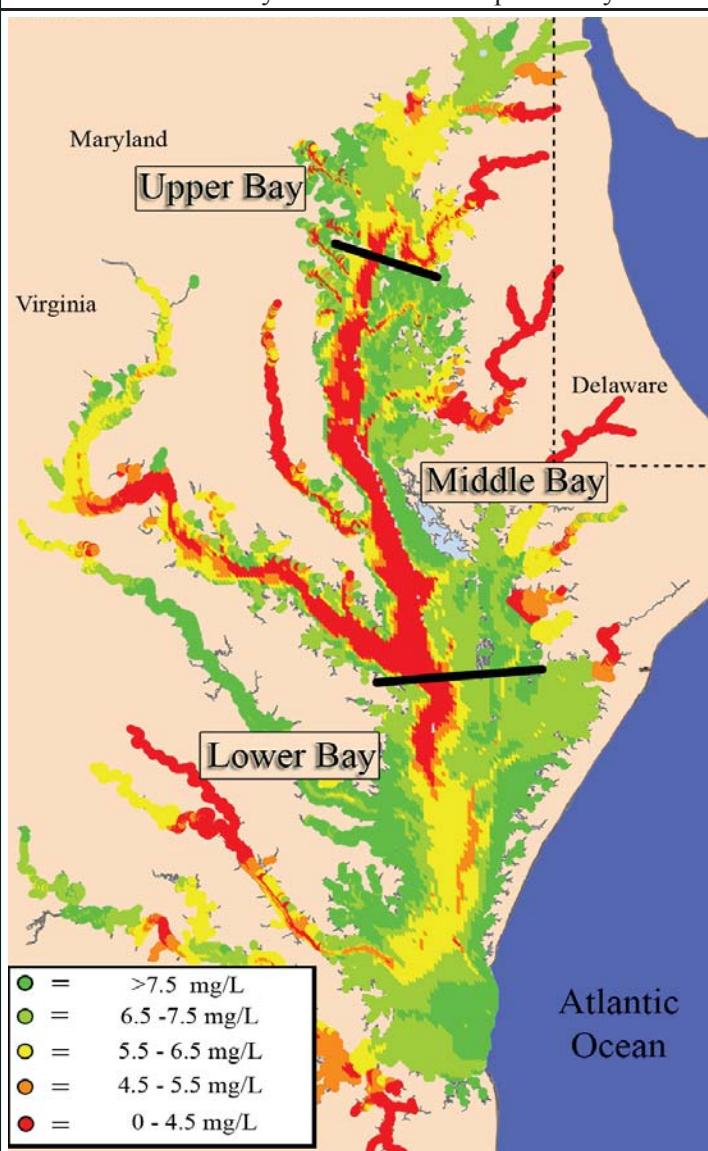
UC = Unclear results. Represents approximately 35% of significant results.

NS = Non significant results.

KEY FINDINGS

Table 1 shows the modeled parameter estimates and their respective significance for each region studied and for all eight variables included in the model.

Figure 2. Map of average bottom water dissolved oxygen concentrations for July 2006 in the Chesapeake Bay.



- The 'middle bay' is most susceptible to low DO concentrations and as the model predicts, has the lowest expected striped bass catch of the sub-regions where the model was significant (Figure 2).
- It appears that the striped bass are migrating out of the areas of low DO concentrations and are being caught in larger numbers in regions where the DO concentrations are higher.
- When significant, the majority (55%) of DO cluster and frequency analysis followed expected relationships of low catch corresponding to low DO and high catch corresponding to high DO (Table 2).
- The change in expected striped bass catch between 2 mg/L to 5 mg/L DO for the entire Chesapeake Bay represents an increase of 149.4% (Table 3). For the 'upper bay' the change in expected striped bass catch between 2 mg/L to 5 mg/L DO represents an infinite increase since at 2 mg/L the expected catch is 0 (Table 3).
- Combined results point toward a possible optimum DO range for catching striped bass in the Chesapeake Bay, ranging around 8-9 mg/L DO.

A more detailed discussion of these findings can be referenced in Mason (2008).

CONCLUSIONS

Increasingly degraded DO conditions, caused by anthropogenic sources, in the Chesapeake Bay over the past century have been negatively impacting human uses of the Bay, including recreational striped bass fishing. For recreational striped bass fishing these losses impact where, when, and if fishermen will catch a fish.

Table 3. Striped bass expected fish catch (per angler per trip) results at mean and predictive conditions.

System/Region	Expected Fish Catch at Mean DO Conditions	Expected Fish Catch at 5 mg/L	Expected Fish Catch at 2 mg/L DO	Percent Increase from 2 to 5 mg/L
Chesapeake Bay*	(mean = 9.28 mg/L) 5.85	2.03	0.67	149.4
Upper Bay*	(mean = 8.35 mg/L) 9.90	3.98	0	Infinite
Middle Bay*	(mean = 7.49 mg/L) 0.25	0	0	0
Long Island Sound**	(mean = 7.18 mg/L) 2.75	2.77	2.71	2.1
Patuxent River**	(mean = 5.99 mg/L) 7.63	6.27	2.16	65.5
Potomac River**	(mean = 4.53 mg/L) 4.07	4.55	1.45	68.1

* = Results from Mason 2008 (full years 2000-2006). ** = Results from Bricker et. al. 2006 (August of 2002).

Development of a human-use indicator model that describes the effect of water quality on recreational striped bass catch in the Chesapeake Bay allows for the more precise quantification of low DO's effect on fish catch. These improved models determine optimum DO for striped bass recreational catch in the Chesapeake to be in the range of 8-9 mg/L. Positive relationships between increased DO and catch are seen in the majority of statistical analysis for the Chesapeake. The predictive capability of the model also allows coastal managers to better determine where resources, further research, and remediation will have the greatest returns.

For the series of non-parametric analysis 55% followed expected trends of increasing catch with increasing DO while 10% had inverse relationships (Table 2). The remaining 35% of analysis had unclear results. According to the Poisson distribution multivariate model when DO is increased from 2 to 5 mg/L DO over the whole Chesapeake Bay there is a corresponding increase in striped bass catch of 149.4% (Table 3).

Although this study demonstrates well that degraded DO conditions impair recreational striped bass catch, there are many other human uses that can be affected by degraded water quality. Understanding the relationships between human uses such as swimming, boating, and fishing for fish species other than striped bass are also important and should be studied in future assessments. Improved modeling of multiple human uses of coastal waters will allow for improved management and policy, as well as making estuarine restoration

a priority.

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CHAPTER 17:

Modeling Hydroclimate Effects on Fish Habitat to Forecast Chesapeake Bay Striped Bass Production



Edward J. Martino*, Bob Wood, and Xinsheng Zhang.

National Centers for Coastal Ocean Science,

Center for Coastal Environmental Health and Biomolecular Research, Cooperative Oxford Laboratory

*Corresponding author, ed.martino@noaa.gov, 410-226-5193 (phone), 410-226-5925 (fax)

BACKGROUND

Dynamics of populations cannot be fully understood without improved understanding of stochastic environmental effects (Fogarty, 1993). Environmental variability that is not considered or accounted for in stock-recruitment models results in poor model fits (Figure 1). The poor fits potentially can be improved by incorporating environmental parameters into stock-recruitment and other assessment models.

Reproductive success and recruitment is critically important as the means to replenish losses of adult fish stocks. Chesapeake Bay striped bass year-class strength varies approximately 100-fold from year to year. Regional climate patterns have been linked to reproductive success and recruitment strength of anadromous fishes, including striped bass, in Chesapeake Bay. For example, inter-annual variability in abundance of young fishes is related to synoptic climatology and resulting hydrological variability during spring months (Wood, 2000; North and Houde, 2001; Jung and Houde, 2002; North and Houde, 2003; Martino and Houde, 2004). Climatology research strongly supports a positive relationship between freshwater flow and recruitment of anadromous fishes (Wood, 2000; Wood and Austin, 2009). Positive

associations between cold-wet spring conditions and recruitment success of anadromous fishes in Chesapeake Bay have been reported in the 1940s (Merriman, 1941) and again in the 1970s (Mihursky *et al.*, 1981). Subsequent research demonstrated that the frequency of favorable and unfavorable climate patterns during spring months act to control abundance of anadromous fish larvae and juveniles, including striped bass (Wood, 2000; Wood and Austin, 2009). Zooplankton prey for early-life stage of fish may explain the links between fish production and climate in Chesapeake Bay. One study focused on Chesapeake Bay striped bass found that the spatial and temporal availability of zooplankton prey controlled fish production (Martino and Houde, 2010).

Figure 1. Effect of including environmental effects in striped bass resource assessment models. Models that include environmental effects explain more of the variability in population production and improve resource assessment and management.

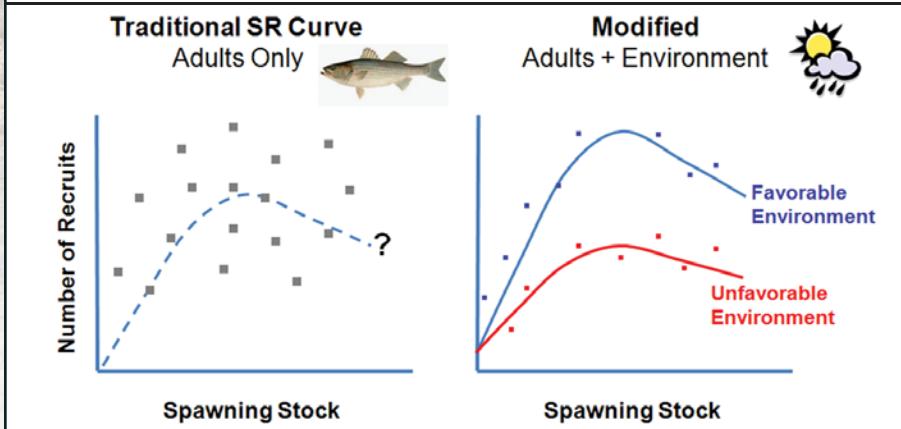
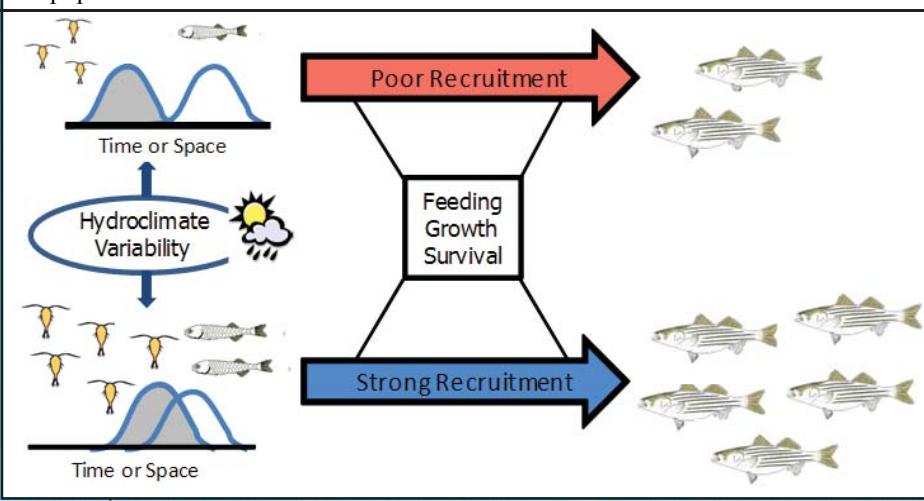


Figure 2. Conceptual illustration of the match-mismatch hypothesis. Hydroclimate variability controls the overlap between young fish and their zooplankton prey. Overlap between fish and their prey enhances survival and the number of adults entering the population.



The working hypothesis for the modeling research described in this chapter proposes that zooplankton prey availability, and the reproductive success and production of striped bass are controlled by inter-annual differences in freshwater flow and temperature (Figure 2).

APPROACH

This research focuses on fish-recruitment model development and validation. Age-0 upper Chesapeake Bay striped bass recruitment indices for the years 1985 through 2010 were calculated by the Maryland Department of Natural Resources (MDNR) as annual geometric mean juvenile catch per seine haul for the months July, August, and September (Figure 3). Daily air temperatures at Baltimore-Washington International (BWI) airport and daily freshwater flows in the Susquehanna River were acquired from the National Climatological Data Center (NCDC) and United States Geological Survey (USGS), respectively. Daily freshwater flow and temperature values were averaged for the March through May period in each year. Multiple linear regression and generalized additive models (Hastie and Tibshirani, 1990) were fit to recruitment and environmental data for the years 1985 through 2005. The models developed here were used to forecast recruitments for the years 2006 through 2010.

Managers and stakeholders are more likely to support models based

on mechanistic links between the environment and fish. Field surveys in the upper Bay are underway to evaluate a suite of biological and hydrographic factors to address a central question, is fish feeding and survival controlled by hydroclimate effects on prey availability? (Figure 4)

We are also evaluating spatial variability in recruitment and differences in environmental effects among spawning locations. Models will be developed for 1) all major Chesapeake Bay spawning locations, and 2) an aggregate bay-wide model representing production for the entire Chesapeake Bay. Requirements of ecosystem-

based fishery management are addressed by evaluating the potential to use these findings for developing indicators of habitat suitability and fish production.

KEY FINDINGS

- A generalized additive model was developed using temperature and freshwater as predictors to evaluate environmental effects on striped bass recruitment for the years 1985-2005.
- The model explained 77% of the variability in upper Chesapeake Bay recruitment (Figure 5).
- The model accurately forecasted recruitments for three recent years 2006, 2007, and 2009.

Figure 3. Map of upper Chesapeake Bay primary study location. Red symbols indicate Maryland Department of Natural Resources fish recruitment monitoring stations.

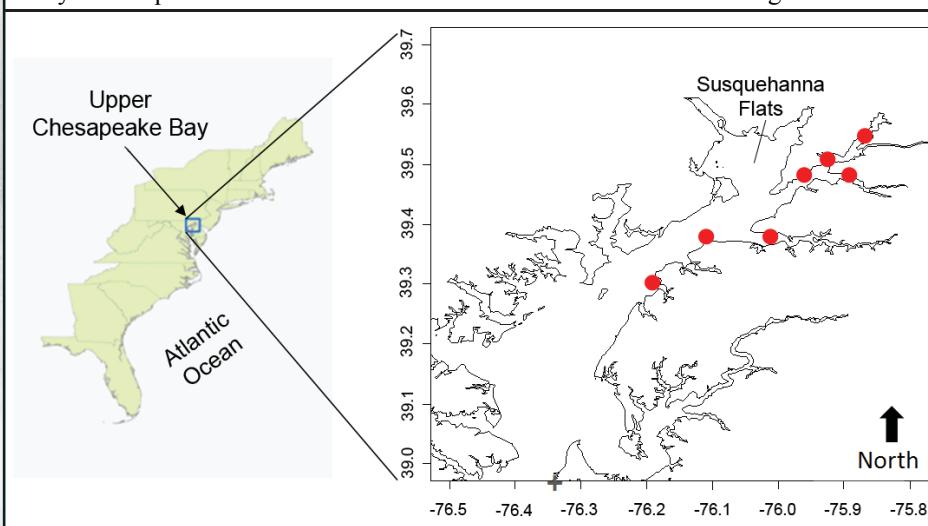
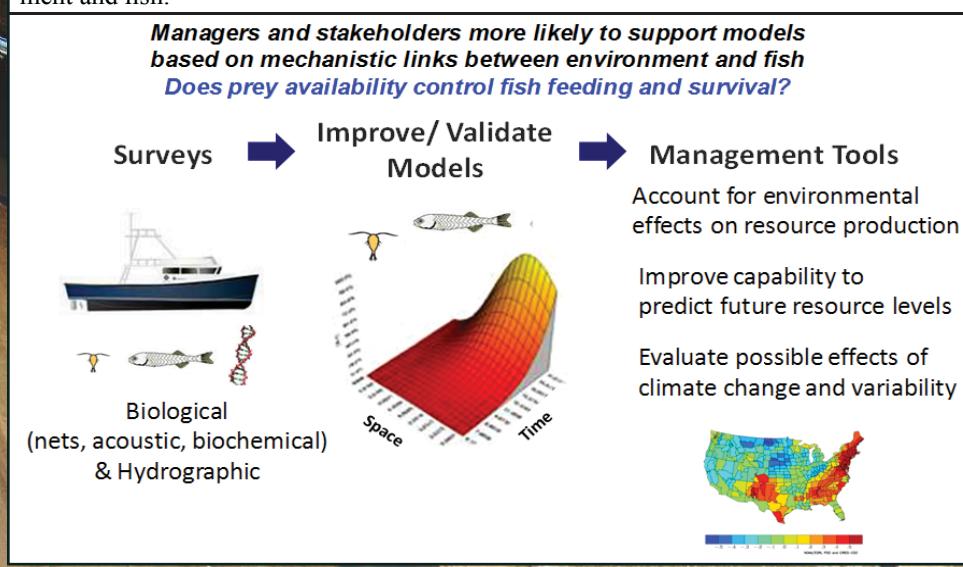


Figure 4. Conceptual illustration of research focused on model improvement and validation. Information from research surveys is used to develop and validate models. Models are used to develop management tools based on mechanistic links between the environment and fish.



- We evaluated the effect of freshwater flow on recruitment using both classification and regression tree analysis and a cubic-spline smoother. Both analyses detected a non-linear relationship between recruitment and flow with a threshold in flow between 60,000 and 70,000 ft³ second⁻¹.
- We successfully forecasted a “below average” striped bass recruitment for 2010. This forecast for “below average” recruitment was supported by our modeling research, and the results from our field surveys in upper Chesapeake Bay. Hydroclimate conditions during winter 2009/2010 were very wet and favorable for high survival of striped bass early-life stages. However, surveys during subsequent cruises in late April through May detected dry hydrological conditions, and ecosystem responses associated with dry conditions including an upbay shift in the location of the salt front and reduced zooplankton concentrations. Further, concentrations of

feeding-stage striped bass larvae were generally low in all but one survey suggesting poor early-life stage survival.

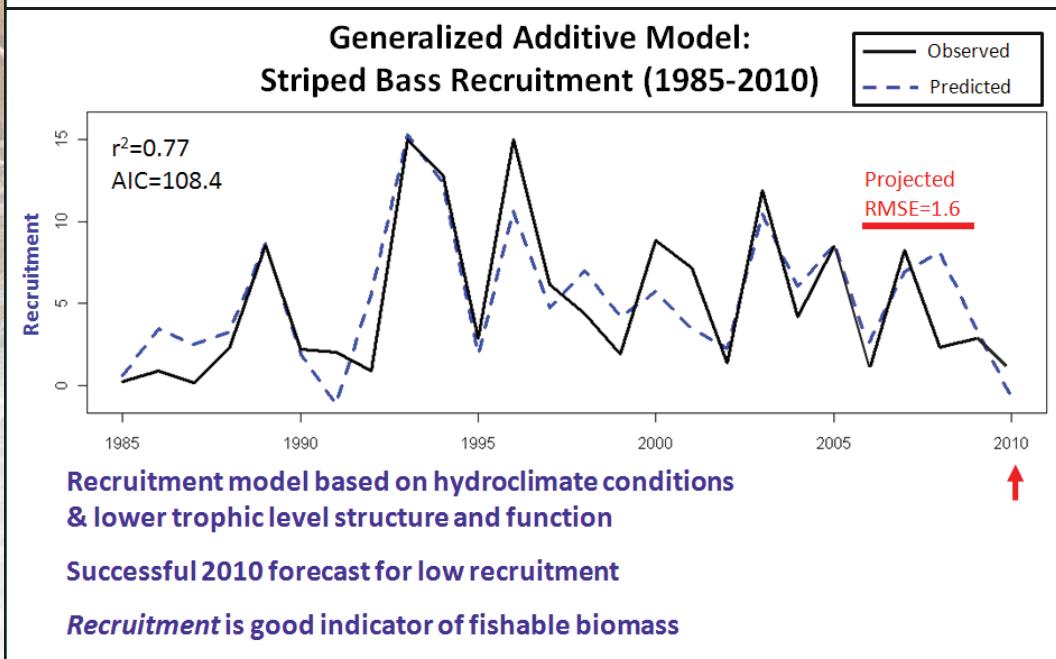
CONCLUSIONS

Models using hydroclimate and habitat effects to forecast population production can improve management and the sustainable use of natural resources by supporting an adaptive-management strategy that responds to environmental variability effects. Successful forecasting of year-class strength provides managers with information on future resource availability. Improved knowledge of resource availability allows informed decisions

to be made on how to fish stocks experiencing favorable or unfavorable environmental conditions 2-3 years prior to their availability in the fishery. The findings here also support the development of ecosystem-based management indicators to inform water resource and other management decisions where fish habitat considerations are necessary.

Downscaled seasonal climate forecasts may enhance our modeling capabilities. We are working with climatologists and hydrodynamic modelers to evaluate the use of downscaled forecasts. The global climate

Figure 5. Observed, predicted, and projected striped bass recruitment in Chesapeake Bay using a generalized additive model.



model is run by the International Research Institute (IRI) at Columbia University and downscaled for the Chesapeake Bay region by our partners at the Earth System Science Interdisciplinary Center at University of Maryland. Seasonal projections of temperature, precipitation, and river discharge have the potential to increase the lead time of recruitment forecasts up to 1 year prior to fishery survey reporting.

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CHAPTER 18:

NOAA's Estuarine Living Marine Resources (ELMR) Program in the Chesapeake Bay

David Moe Nelson*
National Centers for Coastal Ocean Science,
Center for Coastal Monitoring and Assessment

*Corresponding author, david.moe.nelson@noaa.gov, 301-713-3028 x154 (phone), 301-713-4384 (fax)

BACKGROUND

In 1985, NOAA launched a project to develop a consistent data base on the distribution, relative abundance, and life history characteristics of ecologically and economically important fishes and invertebrates in the Nation's estuaries. The project was developed by the Biogeography team (now a branch within NCCOS' Center for Coastal Monitoring and Assessment), and has been conducted cooperatively with NOAA's National Marine Fisheries Service (NMFS) and other agencies and institutions.

The rationale for the project was based on a few key premises:

- Estuaries are among the most productive natural systems and have been shown to be important nursery areas that provide food, refuge from predation, and valuable habitat for many species.
- Estuarine organisms that support important commercial and recreational fisheries include bivalves, decapods, and a variety of finfish.
- In spite of the well documented importance of estuaries to fishes and invertebrates, few sampling programs collect fishes and invertebrates with identical methods across groups of estuaries within a region, and most existing estuarine fisheries data cannot be

compared among estuaries because of the variable sampling strategies

- Much of the distribution and abundance information for estuarine-dependent species (i.e., species that require estuaries during their life cycle) is for offshore life stages and does not adequately describe estuarine distributions.

Because many species use both estuarine and marine habitats during their various life stages, information on their distribution, abundance, temporal utilization and life history characteristics were needed to understand the coupling of estuarine, nearshore, and offshore habitats. Consequently, the ELMR program was developed to integrate disparate information on these species and their associated habitats into a useful, comprehensive and consistent format.

The Nationwide ELMR data base was completed in 1994, and includes information for 153 species found in 122 estuaries and coastal embayments. The data base is divided into five study regions - West Coast, Gulf of Mexico, Southeast, Mid-Atlantic, and North Atlantic. Data include the monthly relative abundance of each species' life stage by estuary for three salinity zones (sea-water, mixing, and tidal fresh), as identified in NOAA's National Estuarine Inventory (NEI) Data Atlas-Volume I and supplement (NOAA 1985). For each species,

Table 1. The Chesapeake Bay and eight sub-estuaries in the ELMR Mid-Atlantic study, and presence/absence of tidal fresh, mixing, and seawater salinity zones. The ELMR Mid-Atlantic study included a total of 22 estuaries.

Estuary Name	State(s)	Tidal Fresh Zone	Mixing Zone	Seawater Zone
Chesapeake Bay	MD VA	present	present	present
Chester River	MD	present	present	
Choptank River	MD	present	present	
Patuxent River	MD	present	present	
Potomac River	MD VA DC	present	present	
Tangier/Pocomoke Sound	MD VA		present	
Rappahannock River	VA	present	present	
York River	VA	present	present	
James River	VA	present	present	

five life stages are considered - adults, juveniles, larvae, spawning, and eggs - with some exceptions based on the unique life histories of some species. Relative abundance is ranked by month for each life stage of each species, in each salinity zone of each estuary.

Since completion of the national ELMR data base in 1994, it has been updated, revised, improved, and applied to specific problems in natural resource management. Regional revisions were completed for the Gulf of Mexico and Southeast in 1998, and a National summary report was published in 2000 (Nelson and Monaco 2000).

METHODS

ELMR information for 61 species in 22 estuaries of the Mid-Atlantic region (Virginia to Massachusetts) was completed in 1994, with the methods and results published in a summary report – *Distribution and abundance of fishes and invertebrates in Mid-Atlantic estuaries* (Stone *et al.* 1994). The initial steps in the project were the selection of the estuaries and species to be studied. Twenty-two Mid-Atlantic estuaries were selected from the *National Estuarine Inventory Data Atlas* (NOAA 1985), including the Chesapeake Bay and eight tributary sub-estuaries (Table 1). The NEI Data Atlas also delineates salinity zones within each estuary, based on annual-and depth-averaged salinity:

- Tidal fresh zone (0.0-0.5 parts per thousand (ppt))
- Mixing zone (0.5-25.0 ppt)
- Seawater zone (> 25 ppt)

These estuarine salinity zones provided the spatial framework for organizing the ELMR data. Some es-

tuaries, such as the Chesapeake Bay mainstem, contain all three salinity zones, but other estuaries may be lacking one or two salinity zones. For example, the eight tidal tributary Chesapeake sub-estuaries are considered to have no seawater zone. Salinity zones that are only seasonally present or are extremely small (<1 km²) were generally omitted from original NEI atlas (NOAA 1985). In the 1990s, the NEI Atlas concept was given

en a digital update, resulting in NOAA's *Coastal Assessment Framework* which integrates national data sets for 138 estuaries within a spatial framework with analytical capabilities (NOAA/NOS 2007). Figure 1 depicts the three salinity zones (Tidal fresh, Mixing, and Seawater) in the Chesapeake Bay and eight sub-estuaries, using a GIS layer taken directly from the *Coastal Assessment Framework*.

Figure 1. Salinity zones (Tidal fresh, Mixing, and Seawater) in the Chesapeake Bay and eight sub-estuaries (NOAA 1985, NOAA/NOS 2007).



In the Mid-Atlantic region, 61 species of fishes and macroinvertebrates were selected for inclusion in the ELMR data base, based on data availability and four criteria:

- Commercial value: determined by review of catch data and value statistics from NMFS and state agencies.
- Recreational value: determined by relative importance in recreational fisheries.
- Indicator of environmental stress: determined from monitoring programs such as NOAA's National Status and Trends Program (Kimbrough *et al.* 2008).
- Ecological value: based on several attributes including trophic level, relative abundance, and importance as a key predator or prey species.

Table 2 provides the common and scientific names of the 61 species selected for the Mid-Atlantic ELMR study. In some cases, two or more closely related species were considered as a single unit (e.g. skates, *Raja sp.*), primarily because of the lack of species-specific fishery survey data. Note that this list contains several species (e.g. Atlantic salmon) that do not occur in the Chesapeake region.

For the majority of Chesapeake Bay species considered in the ELMR program, growth and development involve a direct progression through several distinct life stages. Accordingly, the ELMR program has compiled information based on five "typical" life stages: adult (A), spawning adult (S), juvenile (J), larvae (L) and egg (E). Adults were defined as reproductively mature individuals, while juveniles were defined as immature but otherwise similar to adults. Species with a larval stage typically undergo metamorphosis to the juvenile stage; hence, larvae usually differ from juveniles and adults in form. In addition, most species rely on external fertilization via spawning, when gametes combine externally after being released by males and/or females. Therefore, spawning adults were defined as those releasing eggs or sperm, and

Table 2. Mid-Atlantic ELMR species (n=61)

Common name	Scientific name	Species guild
Blue mussel	<i>Mytilus edulis</i>	Sessile invertebrates
Bay scallop	<i>Argopecten irradians</i>	Sessile invertebrates
American oyster	<i>Crassostrea virginica</i>	Sessile invertebrates
Northern quahog	<i>Mercenaria mercenaria</i>	Sessile invertebrates
Softshell clam	<i>Mya arenaria</i>	Sessile invertebrates
Brown shrimp	<i>Penaeus aztecus</i>	Shrimps and squids
Daggerblade grass shrimp	<i>Palaemonetes pugio</i>	Shrimps and squids
Sevenspine bay shrimp	<i>Crangon septemspinosa</i>	Shrimps and squids
American lobster	<i>Homarus americanus</i>	Large crustaceans
Blue crab	<i>Callinectes sapidus</i>	Large crustaceans
Skates	<i>Raja species</i>	Demersal fishes
Atlantic stingray	<i>Dasyatis sabina</i>	Demersal fishes
Cownose ray	<i>Rhinoptera bonasus</i>	Demersal fishes
Shortnose sturgeon	<i>Acipenser brevirostrum</i>	Demersal fishes
Atlantic sturgeon	<i>Acipenser oxyrinchus</i>	Demersal fishes
American eel	<i>Anguilla rostrata</i>	Demersal fishes
Blueback herring	<i>Alosa aestivalis</i>	Pelagic fishes
Alewife	<i>Alosa pseudoharengus</i>	Pelagic fishes
American shad	<i>Alosa sapidissima</i>	Pelagic fishes
Atlantic menhaden	<i>Brevoortia tyrannus</i>	Pelagic fishes
Atlantic herring	<i>Clupea harengus</i>	Pelagic fishes
Bay anchovy	<i>Anchoa mitchilli</i>	Shallow water fishes
Channel catfish	<i>Ictalurus punctatus</i>	Demersal fishes
Rainbow smelt	<i>Osmerus mordax</i>	Pelagic fishes
Atlantic salmon	<i>Salmo salar</i>	Pelagic fishes
Atlantic cod	<i>Gadus morhua</i>	Demersal fishes
Haddock	<i>Melanogrammus aeglefinus</i>	Demersal fishes
Atlantic tomcod	<i>Microgadus tomcod</i>	Demersal fishes
Pollock	<i>Pollachius virens</i>	Demersal fishes
Red hake	<i>Urophycis chuss</i>	Demersal fishes
Oyster toadfish	<i>Opsanus tau</i>	Demersal fishes
Sheepshead minnow	<i>Cyprinodon variegatus</i>	Shallow water fishes
Killifishes	<i>Fundulus species</i>	Shallow water fishes
Silversides	<i>Menidia species</i>	Shallow water fishes
Northern pipefish	<i>Syngnathus fuscus</i>	Shallow water fishes
Northern searobin	<i>Prionotus carolinus</i>	Demersal fishes
White perch	<i>Morone americana</i>	Pelagic fishes
Striped bass	<i>Morone saxatilis</i>	Pelagic fishes
Black sea bass	<i>Centropristes striata</i>	Pelagic fishes
Yellow perch	<i>Perca flavescens</i>	Pelagic fishes
Bluefish	<i>Pomatomus saltatrix</i>	Pelagic fishes
Pinfish	<i>Lagodon rhomboides</i>	Demersal fishes
Scup	<i>Stenotomus chrysops</i>	Demersal fishes
Spotted seatrout	<i>Cynoscion nebulosus</i>	Demersal fishes
Weakfish	<i>Cynoscion regalis</i>	Demersal fishes
Spot	<i>Leiostomus xanthurus</i>	Demersal fishes
Northern kingfish	<i>Menticirrhus saxatilis</i>	Demersal fishes
Atlantic croaker	<i>Micropogonias undulatus</i>	Demersal fishes
Black drum	<i>Pogonias cromis</i>	Demersal fishes
Red drum	<i>Sciaenops ocellatus</i>	Demersal fishes
Mullets	<i>Mugil species</i>	Demersal fishes
Tautog	<i>Tautoga onitis</i>	Demersal fishes
Cunner	<i>Tautogolabrus adspersus</i>	Demersal fishes
American sand lance	<i>Ammodytes americanus</i>	Shallow water fishes
Gobies	<i>Gobiosoma species</i>	Shallow water fishes
Atlantic mackerel	<i>Scomber scombrus</i>	Pelagic fishes
Butterfish	<i>Peprilus triacanthus</i>	Pelagic fishes
Summer flounder	<i>Paralichthys dentatus</i>	Demersal fishes
Windowpane flounder	<i>Scophthalmus aquosus</i>	Demersal fishes
Winter flounder	<i>Pleuronectes americanus</i>	Demersal fishes
Hogchoker	<i>Trinectes maculatus</i>	Demersal fishes

larvae and eggs included most early life history stages.

However, some species depart from this typical life stage scheme in that spawning is replaced by mating (M), i.e. the transfer of gametes internally between male and female. This reproductive mode differs from spawning in that it often involves specialized copulatory organs (e.g. pelvic claspers in skates) and does not always result in the immediate fertilization of eggs (e.g. spermatophore retention in American lobster and blue crab). Two Mid-Atlantic species (Atlantic stingray and cownose ray) are live-bearers and thus distinguished by a parturition (P) stage, but no egg or larval stage.

ELMR project staff conducted exhaustive literature reviews and data searches to collect existing information on species distribution and abundance. A data sheet was developed for each species in each estuary to facilitate the review and presentation of the information. Data compiled for each species/life stage included: (1) the salinity zone it occupies (seawater, mixing, tidal fresh), (2) its monthly distribution in those zones, and (3) its relative abundance in those zones.

Existing data, published research, and the field experience of local and regional reviewers provide the basis for reasonably accurate synoptic abundance rankings. For well-studied species, quantitative data were used to estimate the relative abundance. The integration of quantitative data and expert review resulted in the final level of abundance assigned to a species. Expert review by regional fisheries scientists complemented the quantitative studies, and greatly increased the reliability of species relative abundance information. The six relative abundance categories are defined as:

- Highly Abundant: species is numerically dominant relative to other species within a guild.
- Abundant: species is often encountered in substantial numbers relative to other species in a guild.
- Common: species is generally encountered, but not in large numbers; distribution may be patchy.
- Rare: species is present, but not frequently encountered.
- Not Present: species or life stage is not found, questionable data as to identification of species, or recent loss or degradation of habitat suggests absence.
- No Information Available: no data available, and

after expert review it was determined that even an educated guess would not be appropriate.

These relative abundance categories were intended to simulate the categories routinely used by fisheries biologists, and is readily understandable by field biologists, fisheries managers, and academic scientists alike. The abundance of a species life stage was considered relative to that of the same life stage of other similar species. Similar species were considered to be those having similar life modes and gear susceptibilities (e.g. skates and flounders, bluefish and striped bass). From the ELMR species list, several groups, or guilds, of species were derived, listed along with each species in Table 2. These guilds are:

- Sessile Invertebrates
- Shrimps and Squids
- Large Crustaceans
- Shallow Water Fishes
- Pelagic Fishes
- Demersal Fishes

Figure 2 depicts the data sheet for bay anchovy (*Anchoa mitchilli*) in Chesapeake Bay, with relative abundance rankings by life stage, salinity zone, and month. In addition, each row of information is assigned a “data reliability” ranking, based on these criteria:

- Highly certain: considerable sampling data available. Distribution, behavior, and preferred habitats well documented within an estuary.
- Moderately certain: some sampling data available for an estuary. Distribution, preferred habitat, and behavior well documented in similar estuaries.
- Reasonable inference: little or no sampling data available. Information on distributions, ecology, and preferred habitats documented in similar estuaries.

Approximately two years were required to develop the 549 data sheets (61 species x 9 estuaries) and consult with regional and local experts for the Chesapeake Bay.

Figure 2. Example of a species/estuary data sheet: Bay anchovy in Chesapeake Bay, with relative abundance rankings by month, life stage, and salinity zone.

Estuary: Chesapeake Bay, Maryland and Virginia														
Species: Bay anchovy (<i>Anchoa mitchilli</i>)														
Life stage	Salinity zone	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec	Data reliability
Adults	Tidal fresh	0	0	0	3	3	4	4	4	3	2	0	0	Highly certain
Eggs	Tidal fresh	0	0	0	0	0	0	0	0	0	0	0	0	Highly certain
Juveniles	Tidal fresh	0	0	0	2	3	5	5	5	3	2	0	0	Moderately certain
LARVAE	Tidal fresh	0	0	0	0	0	0	0	0	0	0	0	0	Highly certain
Spawning	Tidal fresh	0	0	0	0	0	0	0	0	0	0	0	0	Highly certain
Adults	Mixing	5	5	5	5	5	5	5	5	5	5	5	5	Highly certain
Eggs	Mixing	0	0	0	2	4	5	5	5	4	2	0	0	Highly certain
Juveniles	Mixing	5	5	5	3	4	5	5	5	5	5	5	5	Moderately certain
LARVAE	Mixing	0	0	0	2	4	5	5	5	4	2	0	0	Highly certain
Spawning	Mixing	0	0	0	2	4	5	5	5	4	2	0	0	Highly certain
Adults	Seawater	5	5	5	5	5	5	5	5	5	5	5	5	Highly certain
Eggs	Seawater	0	0	0	2	4	5	5	5	4	2	0	0	Highly certain
Juveniles	Seawater	5	5	5	2	2	5	5	5	5	5	5	5	Highly certain
LARVAE	Seawater	0	0	0	2	4	5	5	5	4	2	0	0	Highly certain
Spawning	Seawater	0	0	0	2	4	5	5	5	4	2	0	0	Highly certain

25 data sources and references cited

Expert reviewers: Colvoresses, Houde, Luo

Legend:	Not Present	0
	Rare	2
	Common	3
	Abundant	4
	Highly Abundant	5

peake Bay and its eight sub-estuaries. Nearly all of the data sheets were carefully reviewed during consultations or by mail. These consultations complemented the literature and published data sets compiled by NOAA. 759 sources are cited for the entire Mid-Atlantic ELMR study, and 34 regional experts were consulted for the Chesapeake Bay and tidal tributaries, all listed in the Mid-Atlantic summary report (Stone *et al.* 1994). Local experts were especially helpful in providing estuary/species specific information, as well as additional references and contacts.

RESULTS

The 61 species selected in the Mid-Atlantic region are generally of the cold-temperate fauna of the Virginian marine biogeographic province. Other selected species have a freshwater origin, such as the yellow perch and channel catfish common in the low-salinity tidal tributaries of the Chesapeake Bay. Diadromous species include Atlantic sturgeon, American eel, alewife, blueback herring, American shad, and striped bass. Table 3 readily conveys the occurrence of ELMR species in the Chesapeake Bay mainstem and eight

tributary sub-estuaries. This table depicts the highest relative abundance of the adult or juvenile life stage of each species, in any month, in any salinity zone within each estuary. Relative abundance rankings are coded as Highly Abundant = 5, Abundant = 4, Common = 3, Rare = 2, and Not Present = 0. The spawning, egg, and larval life stage categories are not considered. For display purposes, ten species in the Mid-Atlantic ELMR list that do not occur in the Chesapeake are not included, primarily northern species such as Atlantic cod and Atlantic salmon. A few eurythermal and euryhaline species such as grass shrimp and silversides are ubiquitous, ranked abundant or highly abundant in the Chesapeake and all sub-estuaries. The ELMR Mid-Atlantic summary report (Stone *et al.* 1994) presents both spatial and temporal summary tables for all of the Mid-Atlantic estuaries to visually depict species distribution and abundance, as well as a summary of data reliability for each row of data recorded.

Caveats of the approach

It is recognized that the ELMR methodology has both strengths and limitations as a means to char-

Table 3. Occurrence of ELMR species in Chesapeake Bay and sub-estuaries.

Species	Chesapeake Bay Mainstem	Chester River	Choptank River	Patuxent River	Potomac River	Tangier/Pocomoke Sound	Rappahannock River	York River	James River
blue mussel	4	0	0	0	0	0	3	3	3
eastern oyster	3	3	3	3	3	3	4	2	4
qua hog	3	0	0	0	0	0	3	4	4
softshell clam	2	3	3	3	3	3	3	2	2
brown shrimp	2	0	0	0	2	2	2	2	2
daggerblade grass shrimp	5	5	5	5	5	5	5	5	5
sevenspine bay shrimp	3	3	3	3	3	3	3	3	3
American lobster	2	0	0	0	0	0	0	0	0
blue crab	5	5	5	5	5	5	5	5	5
skates	3	0	0	0	0	0	0	0	0
Atlantic stingray	2	0	0	0	0	0	2	2	2
cownose ray	4	3	3	3	3	3	3	3	3
Atlantic sturgeon	2	0	0	0	2	2	2	2	2
American eel	4	3	3	3	3	3	3	3	3
blueback herring	4	3	3	3	4	4	3	3	3
alewife	4	3	3	3	4	4	3	3	3
American shad	3	3	3	2	3	3	3	3	3
Atlantic menhaden	5	5	5	5	5	4	5	5	5
Atlantic herring	3	0	0	0	0	0	2	2	2
bay anchovy	5	5	5	5	5	5	5	5	5
channel catfish	3	3	3	3	3	3	3	3	3
red hake	3	0	0	0	0	0	2	2	2
oyster toadfish	3	3	3	3	3	3	3	3	3
sheepshead minnow	4	4	4	4	4	4	4	4	4
killifishes	5	5	5	5	5	5	5	5	5
silversides	5	5	5	5	5	5	5	5	5
northern pipefish	3	3	3	3	3	3	3	3	3
northern searobin	4	0	2	2	2	2	2	2	2
white perch	4	4	4	4	4	3	4	4	4
striped bass	3	3	3	4	4	3	3	3	3
black sea bass	3	2	2	2	2	3	2	2	3
yellow perch	3	3	3	3	3	2	3	3	3
bluefish	4	3	3	3	4	4	4	4	4
pinfish	3	0	0	0	0	0	0	0	3
scup	4	0	0	0	0	2	0	2	2
spotted seatrout	3	3	3	3	3	3	3	3	3
weakfish	3	3	3	3	3	3	3	3	3
spot	4	3	4	3	3	4	4	4	4
northern kingfish	2	0	0	2	2	2	2	2	2
Atlantic croaker	4	3	3	3	3	3	4	4	4
black drum	3	2	3	2	3	3	3	3	3
red drum	3	2	2	2	3	3	3	3	3
mullets	3	0	0	2	2	2	2	2	2
tautog	3	2	2	2	2	3	3	3	3
gobies	4	4	4	4	4	4	4	4	4
Atlantic mackerel	2	0	0	0	0	0	2	2	2
butterfish	3	0	2	2	2	2	2	3	3
summer flounder	3	3	3	3	3	3	3	3	3
windowpane flounder	3	0	0	0	0	3	0	2	2
winter flounder	2	2	2	2	2	2	2	2	2
hogchoker	5	5	5	5	5	5	5	5	5

acterize living marine resources. Some of the strengths of the ELMR methodology include:

- Spatial and temporal framework enables synthesis of information from disparate data sets, published research, and expert knowledge.
- Standardized species lists, estuary lists, and data categories result in a consistent and versatile data set with multiple applications.
- The spatial and temporal framework allows simultaneous overview of many species and estuaries, enabling visualization of emergent properties and patterns of variation.

It is because of these strengths that the ELMR data have proven applicable to a variety of natural resource management issues. However, to achieve consistency within a defined framework, this approach also presents some unique challenges and inherent limitations and necessary caveats. These caveats include:

- Relative abundance rankings cannot be translated to actual densities or abundances of organisms.
- Relative abundance rankings are intended to characterize a “typical” year; therefore, interannual and real-time variations are not encompassed.
- Relative abundance rankings may not be comparable between estuaries and regions.
- Relative abundances can only be compared among species within the same “guild” (see methods discussion).
- If a species is scored as “present” within a salinity zone, this does not necessarily mean that it is present consistently throughout that zone. This is especially important in large estuaries like the Chesapeake, with a “mixing zone” (0.5 to 25 ppt) that extends from north of Baltimore all the way to Hampton Roads.
- Most of the ELMR data were compiled in the early 1990s, so they represent a typical year over ten years ago, and do not capture interdecadal trends.

Because of these strengths and limitations, the

ELMR database can provide a good start at getting an overview of species use of estuarine habitats, but it should be supplemented with more detailed and updated information (trawl and seine survey, etc.), depending on what purpose the information is being used.

ELMR information on the web

Through the 1990s, the results of the regional ELMR studies were published in synoptic summaries such as the Mid-Atlantic report (Stone *et al.* 1994), followed by a National overview report (Nelson and Monaco 2000). In order to facilitate the free availability of the original data, NCCOS maintains an online database at <http://biogeo.nos.noaa.gov/products/data/elmr/> where ELMR relative abundance rankings can be queried by region, estuary, species, life stage, and salinity zone. Results can either be viewed as a display table (grid output), or downloaded as tab-delimited ASCII text so that a user can import the data into any word processing, spreadsheet, or database application. Figure 3 illustrates an example query for Atlantic menhaden in Chesapeake Bay.

Applications of ELMR information (in the Chesapeake Region)

Specific applications of the ELMR data to natural resource management issues in the Chesapeake include preparation of Environmental Sensitivity Index (ESI) maps for oil spill response planning (NOAA 2006, 2007), and description of Essential Fish Habitat (EFH) under the Magnuson-Stevens Act (NEFMC 1998, NOAA/NMFS 2010).

Environmental Sensitivity Index (ESI) mapping

Environmental Sensitivity Index (ESI) maps are an integral component of coastal oil spill contingency planning, assessment, and response. They are published and maintained by NOS’ Office of Response and Restoration, and usually published in both digital and hardcopy versions for each individual state. Since the 1990s, the ELMR database and summary reports have been cited as key information sources on the distribution and abundance of living marine resources for most state ESI maps. These include recently updated sets of ESI maps for both Maryland (NOAA 2007) and Virginia (NOAA 2006), including all of the Chesapeake Bay and tributary estuaries. Each ESI map characterizes the estuarine and coastal shoreline for habitat type (e.g. tidal marsh, beach) and ecological sensitivity to the species (fishes and invertebrates, turtles, waterfowl and

Figure 3. Queryable online ELMR database at http://www8.nos.noaa.gov/biogeo_public/elmr.aspx

NCCOS Biogeography Team Coral Reef Ecosystem Assessment and Monitoring Database

Home CCMA Home | About

Estuarine Living Marine Resources Database

A database on the distribution and relative abundance of 153 fishes and invertebrates in 122 estuaries in the continental U.S.. To find out more about the ELMR project, products and how the information was developed, visit the [ELMR](#) project page or contact [David Moe Nelson](#).

To extract data from the ELMR database, select the attributes of interest from the table below. Then select button "Preview Query". To save query results, hit the "Save as Text" button.

Region	Estuary	Species	Life Stage	Salinity Zone
All Regions	All Estuaries	All Species	All Life Stages	All Salinity Zones
GULF OF MEXICO	BARNEGAT BAY	ALABAMA SHAD	ADULTS	>25 ppt
MIDATLANTIC	BUZZARDS BAY	ALEWIFE	EGGS	0-0.5 ppt
NORTH ATLANTIC	CHESAPEAKE BAY	AMERICAN EEL	JUVENILE	0.5-25 ppt

Preview Query Save As Text Clear All

estuary	Common Name	LifeStages	salzone	january	february	march	april	may	june	july	august	september	october	november	december
CHESAPEAKEATLANTIC BAY	MENHADEN	ADULTS	0-5.25 ppt	0	0	0	0	4	5	5	5	5	5	4	0
CHESAPEAKEATLANTIC BAY	MENHADEN	ADULTS	>25 ppt	3	3	3	4	5	5	5	5	5	4	3	
CHESAPEAKEATLANTIC BAY	MENHADEN	ADULTS	0-0.5 ppt	0	0	0	0	0	0	0	0	0	0	0	0
1															

In the query results, the relative abundance codes are defined as follows:

- 5: Highly Abundant
- 4: Abundant
- 3: Common
- 2: Rare
- 0: Not Present

For more information on ELMR metadata, click [here](#).

seabirds, marine mammals, etc.) likely to be present in a given coastal or estuarine area. In addition, each ESI map features a data table which reports the temporal occurrence of each species by life stage. The ELMR data base has proven especially applicable for this purpose, and is cited as a source for the Chesapeake Bay maps in both Maryland and Virginia. Figure 4 depicts an example of an ESI map in the Chesapeake Bay near Annapolis, Maryland (NOAA 2007).

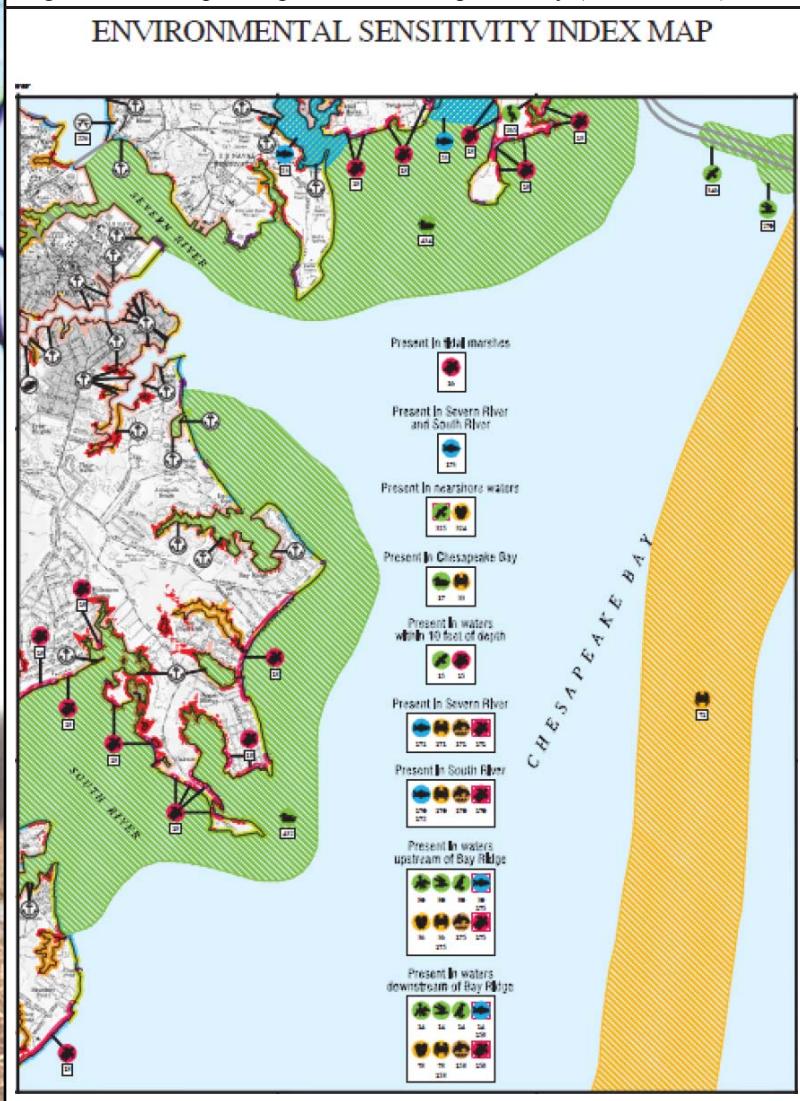
Designation of Essential Fish Habitat (EFH)

The Magnuson-Stevens Fishery Conservation and Management Act was reauthorized in 1996 (NOAA 1996), recognizing the importance of habitat protection

to fishery production. Among its provisions was a requirement that all federal Fishery Management Plans (FMPs) must be amended to include the description, identification, conservation, and enhancement of Essential Fish Habitat (EFH). EFH is generally defined as "waters and substrate necessary to fish for spawning, breeding, feeding, or growth to maturity." Each regional Fishery Management Council (FMC) developed text descriptions and identified the geographic extent of EFH for each species covered by its Fishery Management Plans, with guidance and assistance from NOAA's National Marine Fisheries Service (NMFS).

The geographic extent of EFH for each species was determined by available data on distribution,

Figure 4. ESI map for a portion of Chesapeake Bay (NOAA 2007).



abundance, and habitat-productivity relationships. The types of data sources were classified with respect to their inherent level of detail (NEFMC 1998):

- Level 1: Presence/absence data are available for portions of the species' range.
- Level 2: Habitat-related densities are available.
- Level 3: Growth, reproduction, and survival rates within habitats are available.
- Level 4: Production rates by habitat are available.

In marine waters of the Northeastern continental shelf (including the Mid-Atlantic Bight and Gulf of Maine), the Councils generally used NMFS bottom trawl survey and MARMAP (larval fish) survey data (generally considered Level 2) to develop a ten-minute

square grid-cell based approach to characterizing species distribution and abundance. In estuaries, with the recognition that consistent region-wide inshore survey data were lacking, the ELMR data base was used as a primary source of information on species distribution and abundance (NEFMC 1998). Although the ELMR were considered as "Level 1" (presence/absence) information, the ELMR relative abundance rankings (rare, common, abundant, highly abundant) were used as thresholds in developing different EFH alternatives, and in designating individual estuaries (or portions thereof) as EFH.

Although the Chesapeake Bay is in the Mid-Atlantic region, it provides Essential Fish Habitat for species covered by Fishery Management Plans from all three of the Atlantic FMCs – New England, Mid-Atlantic, and South Atlantic, as well as some Highly Migratory Species such as sandbar shark (*Carcharhinus plumbeus*). Species for which ELMR data were used in defining EFH include red hake, windowpane flounder, Atlantic herring, and skates (*Raja spp.*) in New England FMPs (NEFMC 1998), and summer flounder, black sea bass, scup, bluefish, and butter fish in Mid-Atlantic FMPs (MAFMC 1998a,b,c). The Chesapeake is designated as EFH for several species from South Atlantic FMPs, including red drum, Spanish mackerel, and cobia (SAFMC1998, NOAA/NMFS 2009), although ELMR data were not specifically applied in these designations. Note that cobia and Spanish mackerel are included in the Southeast ELMR regional study (Nelson *et al.* 1991), but not the Mid-Atlantic study (Stone *et al.* 1994).

EFH designations for ELMR species in the Chesapeake and several sub-estuaries are summarized in Table 4. In most cases the original EFH definitions provide more detail – for example, EFH for red hake in the Chesapeake is for adult and juvenile life stages, and only in the Seawater zone of the estuary. In addition, the Chesapeake Bay or portions of it are designated as EFH for some species not included in the ELMR database. For example, the lower Chesapeake is used as a nursery/pupping ground by sandbar sharks, and has been designated as a Habitat Area of Particular Concern (HAPC) (NOAA/NMFS 2009, 2010). The Magnuson-Stevens Act was re-authorized again in 2007, with the existing EFH designations for Chesapeake Bay species

remaining largely intact (NOAA/NMFS 2007, NEFMC 2007).

Future Work

The ELMR database is maintained by Biogeography Branch within NCCOS' Center for Coastal Monitoring and Assessment of the National Ocean Service, with the overall goal to address three basic questions about estuarine and coastal species and habitats:

- What are the distribution, abundance and life history characteristics of estuarine and coastal marine species?
- What is the spatial extent of various estuarine, coastal and marine habitats?
- What are the functional relationships between species and their associated habitats?

The information generated by NOAA's ELMR Program has proven useful for a range of natural resource management applications. However, this information is now well over ten years old. Therefore, CCMA is now considering several possible updates and improvements to the approach. These include:

- Update and improve the ELMR data base on a regional basis, using analysis of available fishery-in-

dependent survey data coupled with expert review. Updates were completed for the Gulf of Mexico, North Carolina, and Massachusetts in the late 1990s.

- The ELMR project relied on estuarine salinity zones as the sole spatial habitat variable. This approach could be improved by refining the spatial characterization of habitats for parameters including bathymetry, substrate, temperature, as well as salinity, using GIS to map these parameters.
- Describe the association between species and their habitats by applying Habitat Suitability Modeling (HSM) and Habitat Affinity Index (HAI) methodologies, and conduct targeted field research to validate species habitat suitability models.
- Make products and services available by publishing summary reports and analytical papers, and ensuring that they are available via the web.
- Develop a web-based mapping capability for linking ELMR data with suitable habitat base layers, using ArcServer or other platform.
- Adapt the approach to other areas such as inshore coastal marine waters, where good fishery independent survey data may be available.

Table 4. Mid-Atlantic ELMR species for which the Chesapeake Bay and sub-estuaries have been designated as EFH based on ELMR relative abundance rankings. "EFH" indicates that at least one salinity zone (Seawater, Mixing, Tidal Fresh) of the estuary has been designated as EFH for at least one life stage (Adults, Juveniles, Larvae, or Eggs) of the species. "FMP reference" identifies which Federal Fishery Management Plan amendment provided the original EFH definition.

Species	Chesapeake Bay	Chester River	Patuxent River	Choptank River	Potomac River	Tangier / Pocomoke Sound	Rappahannock River	York River	James River	FMP reference
Red hake (<i>Urophycis chuss</i>)	EFH									NEFMC 1998
Windowpane flounder (<i>Scophthalmus aquosus</i>)	EFH	EFH	EFH	EFH	EFH	EFH	EFH	EFH	EFH	NEFMC 1998
Atlantic herring (<i>Clupea harengus</i>)	EFH									NEFMC 1998
Bluefish (<i>Pomatomus saltatrix</i>)	EFH	EFH	EFH	EFH	EFH	EFH	EFH	EFH	EFH	MAFMC 1998b
Butterfish (<i>Peprilus triacanthus</i>)	EFH							EFH	EFH	MAFMC 1998c
Summer flounder (<i>Paralichthys dentatus</i>)	EFH	EFH	EFH	EFH	EFH	EFH	EFH	EFH	EFH	MAFMC 1998a
Scup (<i>Stenotomus chrysops</i>)	EFH									MAFMC 1998a
Black sea bass (<i>Centropristes striata</i>)	EFH								EFH	MAFMC 1998a
Red drum (<i>Sciaenops ocellatus</i>)	EFH						EFH	EFH	EFH	SAFMC 1998
Skate species (Clearnose, Little, Rosette, and Winter skates, <i>Raja</i> spp.)	EFH	EFH	EFH	EFH	EFH	EFH	EFH	EFH	EFH	NEFMC 1998

- Continue to apply available information and methodology to special projects such as Essential Fish Habitat (EFH), Environmental Sensitivity Index (ESI) mapping, etc.

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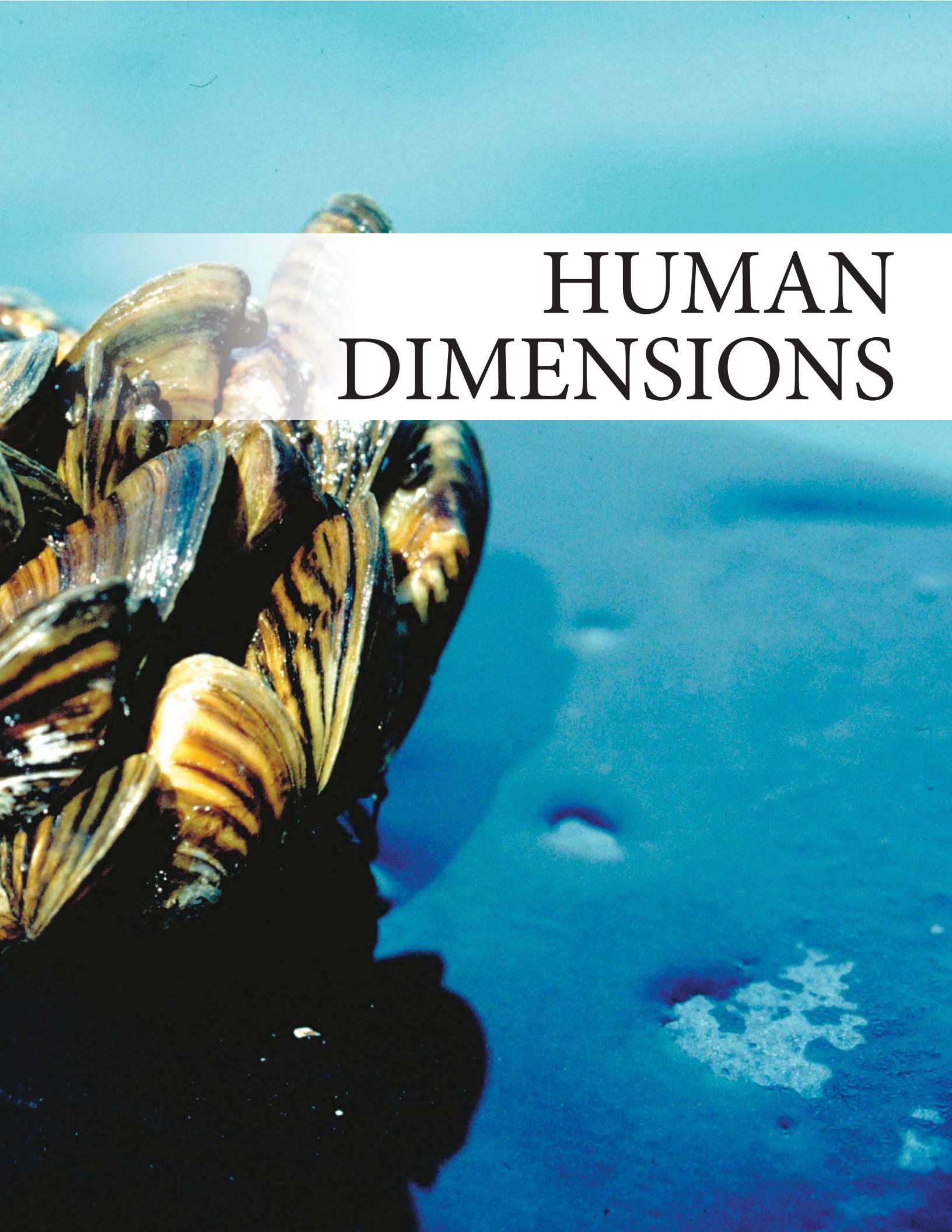
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HABITAT



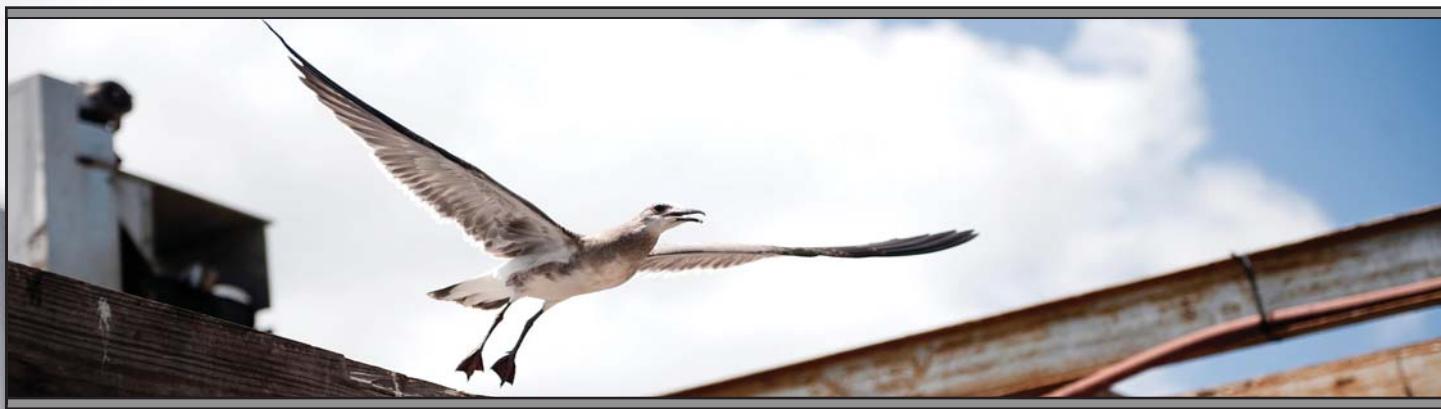




HUMAN DIMENSIONS

CHAPTER 19:

A Social Context for Scientific Understanding of the Chesapeake Bay



Theresa L. Goedeke*, and Cy'Anna Scott.
National Centers for Coastal Ocean Science,
Center for Coastal Monitoring and Assessment

*Corresponding author, theresa.goedeke@noaa.gov, 301-713-3028 x237 (phone), 301-713-4384 (fax)

INTRODUCTION

The Chesapeake Bay is the largest estuary in the continental United States with a total of 11,684 miles of shoreline along the Bay and its tributaries.¹ Although only Maryland and Virginia have shoreline along the Bay proper, the Chesapeake Bay Watershed spans six states, including New York, Pennsylvania, Maryland, Delaware, Virginia, West Virginia, and the District of Columbia. The Bay is home to thousands of plant and animal species, some of which are of tremendous economic, cultural or recreational importance to humans. For over a century, the Bay and its watershed have provided people with valuable ecological services.

The current status of the Bay is inexplicably tied to the decisions, behaviors and activities, some grand and some small, of people. Thus, the health of the Bay depends on both the long-term and everyday choices we make. Moreover, by affecting the health of the Bay through our activities, whether intentionally or not, we are potentially influencing the health, well-being, lifestyle and livelihood of every person who lives, visits or works in the region. In short, the health of the Chesapeake is extremely important to the species that depend upon it, most especially humans.

The Chesapeake Bay and its watershed are deeply intertwined in the history, culture and economy of humans in the Mid-Atlantic Region. For this reason,

understanding the social context of the Chesapeake Bay ecosystem is an important step in understanding the present ecological condition of the Bay and the prospects for its restoration. There are a variety of social, demographic and economic issues that are of significance when considering human influences on ecosystems. Below, to help contextualize the work that NCCOS conducts, we discuss three social dimensions of the Chesapeake Bay Watershed. Specifically, we provide a brief overview of trends in human population change, as well as trends in the agriculture and seafood industrial sectors, all of which are of central importance when considering the status and future of the Bay.

SETTLING THE CHESAPEAKE

Long before the arrival of European colonists, the Chesapeake Bay region was home to the Powhatan, Nanticoke, Piscataway, and other Native peoples whose populations declined dramatically or disappeared after colonization. Beginning in the late 1600s the region became a hub of population and commerce for colonial newcomers because of its diversity of natural features and wealth of natural resources. The Bay region provided people with freshwater, timber, wildlife, fish, shellfish, and fertile land for agricultural production. Additionally, its many tributaries, later augmented with canals and railroads, provided people with transporta-

tion routes linking communities throughout the region. Finally, its natural deepwater inlets provided ports that connected the region to the rest of the world.

By 1790, the year of the first U.S. Census, approximately twenty-seven percent² of the burgeoning American population resided in Maryland and Virginia.³ Not surprisingly, much of the population in these two states was concentrated along the Bay and its tributaries, communities springing up in support of industries like fishing, commerce and trade (Karin 1959). For example, the Port of Baltimore was established in 1706, through which thousands of tons of agricultural and other products arrived or departed for European markets each year. By 1830, the City of Baltimore had expanded to a population of 80,625 people making it the second largest urban center in the nation (Shivers 1995). Baltimore remained one of the ten most populous cities in the U.S. through the 1980 census.⁴

By the turn of the 20th Century, Maryland was ranked as the 26th most populous state with a total population of 1,188,044.⁵ Another fifty years would see Maryland's population double to 2,343,001.⁶ Furthermore, due to expanding population and economic development, the process of urbanization had begun. At the time of the 1910 census more Marylanders lived in urban than rural places.⁷ By 1950, over half (54.4 percent) of Maryland's residents lived in an incorporated place of 2,500 or more inhabitants.⁸ By the 2000 census, 86 percent of Maryland's population lived in an urban area.⁹

Similarly, by the 1900 census, Virginia ranked as the 15th most populous state with a total population of 1,854,184.¹⁰ By 1950, Virginia's population more than doubled to 3,318,080 people. Similar to Maryland, Virginia's urban population also increased over time with 40.3 percent of residents living in an incorporated place of 2,500 or more people by 1950. However, unlike Maryland, the majority of Virginia's population remained in rural areas into the 1950s, although this trend would finally reverse with the 1960 census.¹¹ By the 2000 census, 73 percent of Virginia's population resided in urban areas.¹²

According to U.S. Census Bureau estimates, in 2009 the combined populations of Virginia and Maryland totaled 13,582,068, compared with 5,661,081 in 1950. In 2000, Maryland boasted a population density of 541.9 persons per square mile. Much of the population density in Maryland, and to a large degree in Virginia, has historically been concentrated along the Chesapeake Bay. For example, since the middle 1800s

over half of Maryland's population has resided in a county, including Baltimore City, with shoreline bordering the Chesapeake Bay or one of its major tributaries. Based on Census estimates for 2009, population increased in Maryland's Chesapeake shoreline counties by about fourteen percent from 1990 to 2009. Generally, Maryland's "Western Shore" has had a higher degree of population density because of the metropolitan centers of Baltimore City and Annapolis.

For Virginia, according to the 2000 Census, counties (including the independent cities within those counties) bordering the Chesapeake Bay and major tributaries accounted for 45.9 percent of Virginia's total population. Chesapeake counties and cities in Virginia saw an approximate twenty-six percent increase in population from 1990 to 2009. Areas with the most population increase during this period were Suffolk City along with the counties of James City, Stafford, Prince William and King George, the latter three of which are located on the upper portion of the Potomac River. Of course, the Potomac River makes its way through the District of Columbia as well, which is a major urban population center with an estimated population of 588,373, according the U.S. Census Bureau's 2006-2008 American Community Survey.

Based on an analysis of the socio-demographic aspects of the Chesapeake Bay region for the middle 1990s, Robert McConnell, Professor of Geology at Mary Washington College in Fredericksburg, Virginia, concluded that a human population of about 8 million people "could be readily sustained with the application of modern pollution mitigating technology, concepts of species interdependency, and strict enforcement of applicable laws and regulations" (McConnell 1995, 349). McKendry (2009) reported that some 16.7 million people lived in the Chesapeake Bay Watershed. Additionally, she reported an increase in population across a majority of the counties within the six-state region of the watershed from 1986 to 1996, most especially in Maryland, Virginia and Delaware. In 2006, the Baltimore-Washington D.C. Metropolitan areas had a population density in the range of 767.9 to 9,471.2 persons per square mile of land area (McKendry 2009). Undoubtedly, the Chesapeake Bay region is a densely populated watershed, supporting the lifestyles and livelihoods of millions of people.

McConnell suggested that the human carrying capacity for the Chesapeake Bay watershed "must be considered in the light of applicable technology, per capita consumption, personal awareness and responsi-

bility, and numbers of individuals" (McConnell 1995, 349). In terms of lifestyle, below are a few trends that shed light on the lifestyle and consumption patterns of persons living in the Mid-Atlantic Region:

- The U.S. Census Bureau reports that in 2008 the median household income was \$70,482 for Maryland and \$61,210 for Virginia. That same year, about ten percent of Virginians lived below the poverty level, while eight percent of Marylanders did.¹³
- In 2008, people in the District of Columbia and the six states within the Chesapeake Bay Watershed consumed 13,154.9 trillion Btu of energy from all sources in all end-use sectors, according to the U.S. Energy Information Administration. Also in 2008, per capita energy consumption for Maryland, Virginia and the District of Columbia was 255.7, 322.5 and 305.7 Btu, respectively.¹⁴
- Estimated freshwater withdrawals from both surface and groundwater for Maryland, Virginia and Pennsylvania totaled 17,900,000 million gallons of water per day in 2005 (Kenny *et al.* 2009).
- According to the U.S. Census Bureau, in 2003 Maryland residents spent an average of 30.2 minutes commuting to and from their jobs each day, for a daily commute time of approximately one hour.¹⁵
- In Maryland, approximately fifty-seven percent of all occupied housing units in the state reported having two or more vehicles available to them in 2008, according to the U.S. Census Bureau. Looking at owner occupied housing units alone, seventy percent reported having two or more vehicles available, and just over two percent reported having five or more vehicles available.¹⁶
- According to the American Veterinary Medical Association the total population of pet dogs in the six-states of the Chesapeake Watershed and the District of Columbia was 9,207,000 in 2006 (American Veterinary Medical Association 2007).
- The Maryland Department of Planning estimated that in 2007 there were approximately 430,000 septic systems located on developed parcels of land in the state. The agency projected that about 145,000 additional septic systems would be installed throughout

the state over the next twenty year period.¹⁷

These are just a few of the trends in human lifestyle and consumption patterns (meaning the way we use land, natural resources, energy, goods, products and services in the Mid-Atlantic region) that could have a direct or indirect affect on the Chesapeake Bay Watershed.

In terms of human population change within the Mid-Atlantic region, specifically the Chesapeake Bay Watershed, it is clear that growth in resident human population has been a characterizing trend for the region. In terms of settlement patterns, people in the region predominately live in urban and suburban areas. Additionally, like people across the U.S., persons in Maryland and Virginia have been partial to settling along bodies of water, such as rivers, bays, etc.

When considering the number of people living the region, combined with evidence of current lifestyle choices, it is not difficult to imagine that there are many demands placed upon the region's ecosystems and many stressors (meaning deleterious impacts) for those systems to endure. In order to accommodate millions of people at a moderate to high level of consumption, the resources used and waste produced, technology must exist (as well as be available and effectively used) to abate consequent negative impacts on ecosystems. Alternatively, people, both individually and as a collective, must become more aware of their harmful influence on ecosystems and take responsibility to mitigate or remove those impacts, which may entail some change of lifestyle or adjustment to patterns of consumption. Likely, some combination of both is required to stymie the degradation of the Chesapeake Bay and ensure recovery.

AGRICULTURE IN THE CHESAPEAKE REGION

Historically, Maryland and Virginia, along with the other states within the Chesapeake Bay Watershed, were heavily agricultural and relied to a significant degree on consumptive natural resource industries, such as fishing and logging. Virginia and Maryland were particularly known for the production and exportation of tobacco. By the late 1700s "the tobacco of Virginia and Maryland supplied the world" (Ford 1895, 20). In 1950, Maryland alone produced 35,532,656 pounds of tobacco, while Virginia's harvest reached 124,904,164 pounds.¹⁸ Much wheat was also grown in the region, milled into flour and exported internationally, raw and as baked goods. Other agricultural industries impor-

tant in the region historically included livestock (particularly chickens, cattle and honey bees), grains, hay, vegetables and a variety of orchard fruits.

One of the most dramatic changes in the Chesapeake Bay ecosystem has been the transformation of land from “resource land,” including forested and agricultural lands, to buildings, streets, parking lots and other structures that make life more comfortable, profitable and convenient for people. According to Patrick Jantz, Scott Goetz and Claire Jantz (2005), resource lands within commuting distance to growing urban areas in the Chesapeake Bay Watershed were developed at a greater rate from 1990 to 2000. The authors concluded that sixty-four percent of all land lost to development in the Watershed during this period had formerly been agricultural. Further, they speculated that the social motivation for these development patterns included people’s desire to have “open space, lower housing costs, and more land on which to build,” in addition to the acquisition of “second-homes” (Jantz *et al.* 2005, 822). The U.S. Geological Survey suggested additional factors responsible for sprawling patterns of growth in the region, including “houses on large lots and commercial preferences for less expensive office and retail space” (Phillips 2007, 10).

Both of these suggestions are consistent with findings from J.G. Bartlett and co-authors (2000, 457) who describe the shift of rural population to metropolitan areas, a traditional pattern of human population settlement in recent decades, and the simultaneous trend of “de-concentration” meaning that people are moving from major metropolitan centers to formerly rural areas that are within commuting distance. This latter settlement pattern has led to the conversion of agricultural,

forest, and other resource lands, leading to a sprawl of roads, housing developments, shopping centers, etc. in numerous “edge cities” surrounding metropolitan areas; many of these edge cities are situated in more sensitive coastal areas that hold high amenity and aesthetic appeal for people (Bartlett *et al.* 2000). However, there are certainly some social, economic and environmental costs to this type of develop pattern, such as increased commuting time and energy consumption, for example (Environmental Protection Agency 1998).

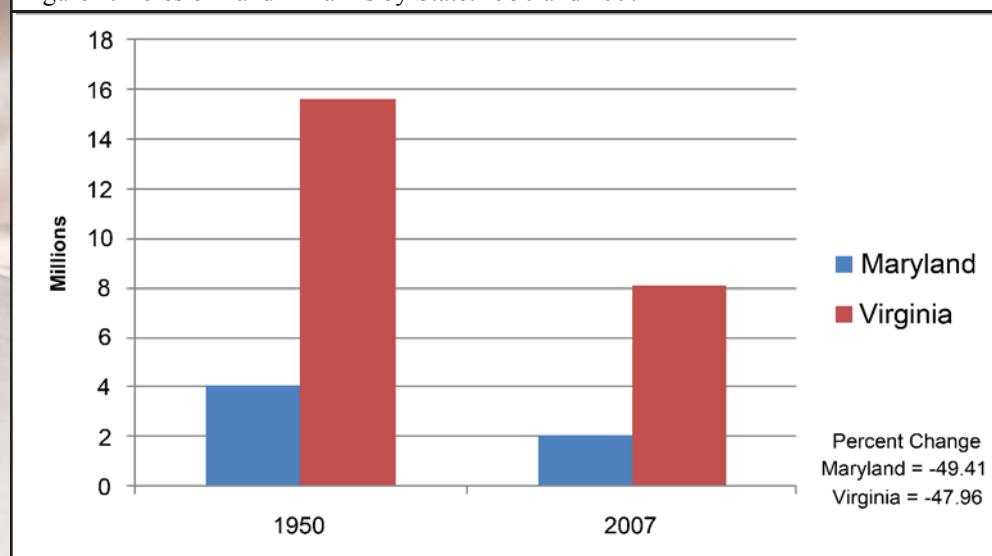
No doubt, one of the most sobering changes over time for the region has been the reduction in agricultural and forested land. Since the first Census of Agriculture in 1900 to the most recent in 2007, both Maryland and Virginia experienced an approximate sixty percent decrease in the amount of land devoted to agriculture. As seen in Figure 1, since 1950 the region has lost nearly ten million acres of farmland, in both states combined. Conversion of agricultural land to residential and business developments means more impervious surfacing across the region, which in turn leads to more pollutant and nutrient inputs into the Chesapeake Bay from leaf litter, vehicle emissions, residential and roadside landscaping (fertilizers), concentrations of urban wildlife and pets, soil erosion, etc (Roberts *et al.* 2009; Roberts & Prince 2010).

Nevertheless, there is still a great deal of land in the region devoted to agricultural production. Maryland, for example, had 2,051,756 acres of land in farms in 2007, with approximately fifty-eight percent of that acreage located in a county bordering the Chesapeake Bay, primarily on the Eastern Shore. In 2007, Virginia had 836,165 acres of farmland located in its counties and cities bordering the Chesapeake Bay, accounting for

about ten percent of the state’s agricultural lands. According to the 2007 Agricultural Census, agricultural producers in the six-state Chesapeake Bay region continue to raise a variety of crops, including corn, wheat, tobacco, oats, etc., along with livestock, particularly cattle and chickens.

Industrial agriculture, of course, is known for its chemical inputs and waste production. For example, in 2007, Maryland farmers applied manure, commercial fertilizers, lime or other

Figure 1. Acres of Land in Farms by State: 1950 and 2007



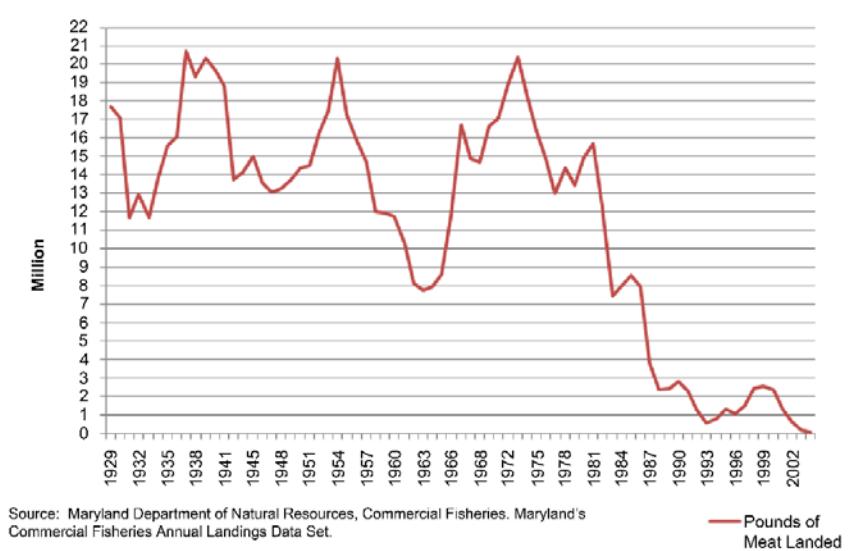
soil conditioners to 1,327,037 acres of agricultural land in the state, and applied chemical pesticides to 1,395,016 acres of farmland.¹⁹ The Maryland Pesticide Network compiled existing data on the volume of pesticide use in Maryland and estimated that, of the top twenty most commonly used pesticides, some 10,722,796 pounds of active pesticide ingredient were applied in the state by farmers, private persons, businesses and government agencies in 2004.²⁰ In terms of waste, livestock production necessarily means that large quantities and concentrations of animal waste will be a by-product of a farming operation. For example, one beef cow has been estimated to produce 11.50 tons of manure annually, while dairy cows produce approximately 15.24 tons of manure annually per animal unit, which is .74 (Hansen 2006). Thus, Maryland's approximately 195,000 beef cattle and 55,000 dairy cows²¹ in the state together produce roughly 2,355,797 tons of manure, annually. The challenge is to manage agricultural production in a way that significantly reduces the amount of pollutants, whether chemical or manure, that reach the Bay.

THE SEAFOOD INDUSTRY

The Chesapeake Bay has long been known for its seafood production, most notably for the harvest, canning and exportation of oysters, fish and fish products, such as oil made from menhaden (Blackford 1895). Oysters, most especially, were a hallmark product of the region. According one 19th century author, "cove" oysters from the Chesapeake Bay were "famous for [their] size and quality" (Judge 1895, 397). In Maryland, in 1895, "The total weight of the [oyster] product from the water was 590,454,369 pounds, worth \$19,023,474" (Blackford 1895, 394). James B. Engle, a federal scientist specializing in shellfish ecology, described Baltimore as the "oyster capitol of the nation" throughout the 1800s (Engle 1964). Not surprisingly, in 1890 twenty-two percent of the nation's 163,348 commercial fishermen were employed in Maryland alone (Blackford 1895, 394).

However, overharvest of Chesapeake Bay oysters was recognized early in the region's history. By the late 1800s, an expert wrote: "The oyster-beds of Maryland and Virginia were at one time deemed inexhaustible, but constant dredging for oysters, the quantity

Figure 2. Total Annual Landings for Commercial Harvest of Oysters in Maryland: 1929 to 2004.



desired being on an ever ascending scale, showed that the beds of Chesapeake Bay were unable to stand the demands made on them" (Blackford 1895, 392). Annual oyster harvest in Maryland and Virginia, which reached over 70 million pounds in Maryland and more than forty million pounds in Virginia in 1880, began to decline around the turn of the 20th century (Engle 1964). By the early 1900s, oyster harvests in both states had plummeted to below approximately twenty million pounds of oysters per year. As seen in Figure 2, by the 1960s oyster landings in Maryland dipped below ten million pounds, rose slightly in the late 1960s and 1970s, and then dove once again in the early 1980s, not to recover substantially.

According to Engle (1964), the decline in landings of Chesapeake Bay oysters was due to a number of problems, such as overharvest, water pollution, depredation and disease. In 2008, fishers landed only 249,000 pounds of oysters in Maryland²² and oyster harvesting in Virginia is no longer a viable industry. Over the decades, other fisheries in the Chesapeake, such as crab, finfish and other shellfish, have experienced fluctuations in the availability of species for harvest or in the size and quality of product landed.

However, the seafood industry continues to be an important economic sector in Maryland and Virginia. In 2008, Maryland employed 10,946 full and part-time workers in seafood-industry related jobs, while Virginia employed 30,734 workers.²³ In 2008, Maryland watermen landed \$73,505,000 worth of commercial seafood, including finfish and shellfish, and the value of landings by Virginia fishers was \$145,552,000. In

both states, blue crab is one of the most valuable species commercially harvested from the Bay, while menhaden continues by far to be the most landed commercial seafood product in Virginia.²⁴

THE RELEVANCE OF NCCOS' SCIENTIFIC RESEARCH

To say that the Chesapeake Bay and its watershed are important to the Mid-Atlantic region, its people, cultures, communities and economies, is an understatement to be sure. Both historically and today, the Bay has provisioned people with an array of consumables, served as a sink for our waste and refuse, and provided us with a diversity of recreational and economic opportunities. More than this, life on and around the Bay influenced the development of local and regional culture, giving rise to unique values, traditions and knowledge that once spanned generations, and in many cases still do. The importance of the Bay to people is undeniable, which makes its degradation all the more tragic and lamentable. As it turns out, rather than being an inexhaustible source of ecological goods and services, a myth once held true, years of experience and research have taught us that the Bay is not immune from the pressures of our lifestyles, economies, technologies and policies.

On a grand scale, the problem with the Bay is clear enough. The challenges of curtailing water pollution, restoring wetland and aquatic habitat, and preserving resource lands within the watershed are monumental because they stem from the reality of an expanding human population, and consequent development, as well as our affluent, highly consumptive lifestyles. Neither human population growth nor trends in resource consumption appear to have limit at this time. As science journalist Tom Horton wrote, "Adding more people to the watershed requires a rebalancing of the developed with the natural. Each time the balance is struck anew, we seem to be left with a little more concrete and a little less nature" (Horton 1988, 417).

Our impacts on the Chesapeake Bay, as a society, have been dramatic over the decades. For instance, since covering the land with impervious surfaces, like concrete, asphalt and roofs that do not allow water to slowly percolate through the soil, rains that once rejuvenated the estuaries with freshwater instead sweep into the Bay the debris, trash and chemicals left behind daily by millions of people living in the watershed. Additionally, millions of people create billions of gallons of sewage composed of human waste, household chemi-

cals, pharmaceuticals, bacteria, viruses, parasites and plethora of other components that, whether treated or otherwise, ultimately discharge into groundwater and tributaries to the Chesapeake Bay. Finally, the region's agricultural producers, in a quest to grow food for the nation in the most efficient and profitable manner possible, house large concentrations of animals, plow and graze the land, and apply chemicals to crops and livestock. Again, rains that once replenished the Bay now routinely carry sediment, animal waste, herbicides, pesticides and other pollutants into its waters.

Hundreds of years of human alterations to the Bay, such as overharvest of species and water pollution, are now compounded by more recently recognized problems, like invasive species and sea level rise. Moreover, the cumulative or combined effect of stressors requires a new approach to both understanding and addressing ecological issues. For example, how do shellfish populations fare when they have large burdens of both parasites and heavy metals or other chemical contaminants? How well will shellfish already suffering with heavy burdens of both parasites and chemical contaminants adapt if their habitat is further degraded as a result of sea level rise? What does all of this mean for the health and well-being of people? With less and less "nature" we face more and more complicated questions about how we as a society continue to compromise the Bay and how we can successfully sustain, restore and improve those ecological systems that we have depended upon for so long. However, with limited financial resources available to tackle the Bay's many problems, research is required to prioritize and guide policy and management solutions.

The research that NCCOS scientists have undertaken related to the Chesapeake Bay has contributed greatly to discussions about the status of the Bay, which is of vital importance to those who live, work and play in the region. For example, research documenting the levels of contaminants in the water, sediment and organisms provides people with information about which species, including humans, are at risk for exposure and potential harm. Additionally, this research informs natural resource managers about which contaminants are most prevalent in the Bay and where they are found so that policy might be strengthened to address these issues. The research conducted by NCCOS scientists is very important from a management and policy making perspective because it helps those responsible for improving the Bay to understand more clearly the issues related to water quality, the spatial and temporal varia-

tion of contamination, and the impact of poor water quality on the ecosystem and people.

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⁷Census of Population, 1950.

⁸Census of Population, 1950.

⁹U.S. Census Bureau: Table P2. URBAN AND RURAL [6] - Universe: Total population Data Set: Census 2000 Summary File 1 (SF 1) 100-Percent Data. Note: For the 2000 Census “Urban Area” includes urban clusters (i.e., territory having at least 2,500 people, but fewer than 50,000) and urbanized areas (i.e., population centers with a “general population density of at least 1,000 people per square mile of land area that together have a minimum residential population of at least 50,000 people”).

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